

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 4, 2005, 10:55:59 ; Search time 41322 Seconds
(without alignments)
11908.008 Million cell updates/sec

Title: US-10-076-839A-1
Perfect score: 10155
Sequence: 1 naaaaauuaaaacuucaac.....ucagcuuagcaaggagggn 10155

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_hgt.*

3: gb_in.*

4: gb_cm.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|----------------------|
| 1 | 10153 | 100.0 | 10153 | 14 | AB088221 Papaya le |
| 2 | 10153 | 100.0 | 10155 | 6 | BD171712 Full-leng |
| 3 | 2385 | 23.5 | 9798 | 14 | AB093599 Turnip mo |
| 4 | 2365.2 | 23.3 | 9760 | 14 | AB027007 Japanese |
| 5 | 2363.6 | 23.3 | 9760 | 6 | E59210 Attenuated |
| 6 | 2340.2 | 23.0 | 9757 | 14 | AB016500 Japanese |
| 7 | 2337.2 | 23.0 | 9798 | 14 | AB093597 Turnip mo |
| 8 | 2309.8 | 22.7 | 9798 | 14 | AB093604 Turnip mo |
| 9 | 2308.6 | 22.7 | 9797 | 14 | AB093598 Turnip mo |
| 10 | 2304 | 22.7 | 9797 | 14 | AB093596 Turnip mo |
| 11 | 2303.6 | 22.7 | 9741 | 14 | PPV |
| 12 | 2301 | 22.7 | 9795 | 14 | AY184478 Plum pox vi |
| 13 | 2298.2 | 22.6 | 9798 | 14 | AB093602 Turnip mo |
| 14 | 2294.6 | 22.6 | 9587 | 14 | AJ3131400 Potato vi |
| 15 | 2294.6 | 22.6 | 9795 | 14 | PPNIB |
| 16 | 2292.4 | 22.6 | 9798 | 14 | AB093616 Plum pox po |
| 17 | 2292.2 | 22.6 | 9798 | 14 | AB093615 Turnip mo |
| 18 | 2287.6 | 22.5 | 9798 | 14 | AB093612 Turnip mo |
| 19 | 2287.2 | 22.5 | 9786 | 14 | AF401295 Plum pox |

| | | | | | |
|----|--------|------|------|----|---------------------|
| 20 | 2286.6 | 22.5 | 9798 | 14 | AB093610 Turnip mo |
| 21 | 2286.2 | 22.5 | 9844 | 14 | AY227024 Turnip mo |
| 22 | 2281.8 | 22.5 | 9798 | 14 | AB093601 Turnip mo |
| 23 | 2281.2 | 22.5 | 9798 | 14 | AB093626 Turnip mo |
| 24 | 2280.4 | 22.5 | 9833 | 14 | AB105135 Turnip mo |
| 25 | 2278.8 | 22.4 | 9798 | 14 | AB093622 Turnip mo |
| 26 | 2278.2 | 22.4 | 9786 | 14 | AY028309 Plum pox |
| 27 | 2277.6 | 22.4 | 9598 | 14 | AF543709 Potato vi |
| 28 | 2276.4 | 22.4 | 9598 | 14 | AF401296 Plum pox |
| 29 | 2276 | 22.4 | 9598 | 14 | AF543212 Potato vi |
| 30 | 2275.6 | 22.4 | 9608 | 14 | U42596 Yam mosaic |
| 31 | 2273.8 | 22.4 | 9787 | 14 | X16415 Plum pox vi |
| 32 | 2273.6 | 22.4 | 9786 | 14 | X81083 Plum pox po |
| 33 | 2273.2 | 22.4 | 9798 | 14 | AB093621 Turnip mo |
| 34 | 2271.4 | 22.4 | 9324 | 14 | SMO316084 Scallion |
| 35 | 2270.4 | 22.4 | 9798 | 14 | AB093624 Turnip mo |
| 36 | 2267.4 | 22.3 | 9585 | 14 | AJ296311 Potato A |
| 37 | 2266 | 22.3 | 9798 | 14 | AB093623 Turnip mo |
| 38 | 2265.6 | 22.3 | 9833 | 14 | AY090860 Turnip mo |
| 39 | 2264.8 | 22.3 | 9830 | 14 | TMVCAPP |
| 40 | 2262.4 | 22.3 | 9798 | 14 | AB093625 Turnip mo |
| 41 | 2261 | 22.3 | 9585 | 14 | PVCGA |
| 42 | 2261 | 22.3 | 9798 | 14 | AB093608 Turnip mo |
| 43 | 2260.8 | 22.3 | 9605 | 14 | PV1131403 Potato vi |
| 44 | 2260.4 | 22.3 | 9798 | 14 | AB093617 Turnip mo |
| 45 | 2258 | 22.2 | 9833 | 14 | AB105134 Turnip mo |

ALIGNMENTS

RESULT 1
LOCUS AB088221 10153 bp RNA linear VRL 24-JUL-2003
DEFINITION Papaya leaf-distortion mosaic potyvirus genomic RNA, complete
ACCESSION AB088221
VERSION AB088221.1 GI:33235542
KEYWORDS
SOURCE Papaya leaf-distortion mosaic potyvirus
ORGANISM Papaya leaf-distortion mosaic potyvirus
VIRUSES; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
Potyvirus.

REFERENCE 1
AUTHORS Maoka,T., Kashiwazaki,S., Tsuda,S., Usugi,T. and Hibino,H.
TITLE Nucleotide sequence of the capsid protein gene of papaya
JOURNAL leaf-distortion mosaic potyvirus
MEDLINE Arch. Virol. 141 (1), 197-204 (1996)
PUBMED 96207852
8629948
REFERENCE 2
AUTHORS Maoka,T., Hataya,T., Uyeda,I. and Fukumoto,F.
TITLE The complete nucleotide sequence of Papaya leaf distortion mosaic
virus RNA: isolate variability and the origin of PLDMV

JOURNAL Unpublished
REFERENCE 3 (bases 1 to 10153)
AUTHORS Maoka,T.
TITLE Direct Submission
JOURNAL Submitted (15-JUL-2002) Tetsuo Maoka, National Agricultural
Research Center for Hokkaido Region, Plant Virology Lab. ;
Hitsujiigaoka 1, Toyohira, Sapporo 0628555, Japan
(E-mail:maokat@affrc.go.jp, URL:http://cryo.naro.affrc.go.jp/,
Tel:81-11-857-9278, Fax:81-11-859-2178)

FEATURES
source
1..10153
/organism="Papaya leaf-distortion mosaic potyvirus"
/mol_type="genomic RNA"
/strain="p"
/isolate="J56p"
/isolation_source="The leaf distortion mosaic (LDM)
isolate of PLDMV"
/specific_host="Carica papaya"
/db_xref="taxon:46917"

| | | | |
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| Qy | 7202 | UUAUAACAACGGAAAGGCAUUUGUGGAUUUGCCUUAGUUAGUGUCACUGAUGGAAUUUAUUG | 7261 |
| Db | 7201 | TTAATACAAACGGAAGGACATTGTGGA TTGCCTTTAGTGTACTGATGGATTTATTG | 7260 |
| Qy | 7262 | UAGGAUAUCAUUAUGAUAGAUCUAAGAUAAGCUAUAUAUAUUUUUUCUCGAAUUUGACG | 7321 |
| Db | 7261 | TAGGAATACATAGTTTTAATGAGTCATAAGTAGCAGCATCAATATTATTTTCTCGAACTTTTGACG | 7320 |
| Qy | 7322 | ACGCGUUGAAGCGCAUUAUUAUUAACAAGUUGAAGGAACUGAUAUUGGAGCGACGAUUUGGA | 7381 |
| Db | 7321 | ACGCGTTTTGAAGGCGATTTATTTAACCAAGTTTGAAGGAAC TGAATGGAGCGAGAAATTTGGA | 7380 |
| Qy | 7382 | CUUACAAACGUUAUAUCUGUUAUUGUGGCGCAACAUGAAAA CUUCAGAAUAGUGUCUCCAUGCA | 7441 |
| Db | 7381 | CTTACAACGTTNATACTGTTAGTTGGGCGCAACATGAACCTT CAGGATAGTGCTCCATGCA | 7440 |
| Qy | 7442 | AAGAAUUCUAAAACAAUAAGUUGAUUAGCGCAUUUAUGCA CGGAACCUUGUGUGCGCUCAGA | 7501 |
| Db | 7441 | AAGAAATTCAAAAACAACCTAAGTTGATTAGCACTTATGCA CGGAACCTGTGTGGCTCAGA | 7500 |
| Qy | 7502 | GUAGCAUACAUGUUAUGGUUAUUAUAUACGCUUGAAGGA AUAUUUAAAACGGUUGCAA | 7561 |
| Db | 7501 | GTAGCAATCAAGTTAGATGGTTATATAATCAGCTTTGAAG GAAATTTGANAAGCGGTGCGAA | 7560 |
| Qy | 7562 | CUAUUCCCCAAUACUUUUAUCAAAGCACAUUGUGAAAGG ACGAUGUAAAUUUGUUUGAAU | 7621 |
| Db | 7561 | CTATTCCCATAACTTTGTTACAAGGACACATTTGTAAGAG GACGATGTAAATTTGTTGAT | 7620 |
| Qy | 7622 | UGUAUCUGCAAAACUCGUAUGAAGCGAAUGAGUUUUUA AACCACUGAUGGGUUUCUAUG | 7681 |
| Db | 7621 | TGTATCTGCAAACTCGTAGTGAAGCGAATCAGTTCTTTA AAACCACTGATGGTTTTCTATG | 7680 |
| Qy | 7682 | GGAAGAGCGGUCUCAAACAAGGAGCAUAUAUUAAGGAC CUUAUUAUAUAUCUAUCAGAAA | 7741 |
| Db | 7681 | GGAAGAGCGGTCTCAACAAGGAAGCATACATTAAGGACC TATTATTAATATCTCATCAGAAA | 7740 |
| Qy | 7742 | UACCAUUGGGGAGGUCGACACUCAGAGAGAUUUGAAGA UGACGAGUUGGCGCAAGUCAUGAAA | 7801 |
| Db | 7741 | TACCAATTTGGGAGGTCGACACTGAGAGATTTGNAAGAT GCAGTTGGGCAAGTCATCGAAA | 7800 |
| Qy | 7802 | UUAUGAUGCAAUGGAAACUUUAGGAAUUGCAAGUAUAU CAACCGAUGGACCAGAACUUCUUG | 7861 |
| Db | 7801 | TTATGATGCAATGSAACTTTTAGGGAATGCAAGTATATCA CCGATTTGTGCCAGCATCTTG | 7860 |
| Qy | 7862 | AUCAUUGAACAUGAAACGGCACUGCUGGCGGUUGUA CAUGUGUAAGAAAAAGCGCUACU | 7921 |
| Db | 7861 | AATCATTTGAACATGAAACGGCGACGTGGTGCGTTGTAC AGTGGTAAAGAAAAGCGCGTACT | 7920 |
| Qy | 7922 | UCGAAAAUCCACAUUUGAUGAUCGAAAUCAUJUUCUA CAGCUUAGUUGUCUCCGAUUUAU | 7981 |
| Db | 7921 | TCGAAAAATCCACATTTGATGATCGAAATCATTTTCTAC AGCTAGTTGTCTCCGATTAT | 7980 |
| Qy | 7982 | UCAAGGUGUAUUUGGGAUUUUGGAAUUGGAAGUCUUA AAGCGUAUAUUAAGACCAAUUGAAA | 8041 |
| Db | 7981 | TCAAGSGTGATTTGGGAATTTGGAATGGAAGTCTTAAAG CTGAAATTAAGACCAATTGAAA | 8040 |
| Qy | 8042 | AGGUUGAAGCAAAACAAACCGGAAACAUUICACAGCAG CUCCAUUUGAAAAUUUAUCUUGCGG | 8101 |
| Db | 8041 | AGGTTGAAGCAAAACAAACCGCAACATTCACAGCAGCT CCAAATTTGAAACTTTTACTTTGGCG | 8100 |
| Qy | 8102 | GAAAGGUUUCGUGCAUUAUUAACAACCAAUUUAUGAU CUUUAUUAUGAAUUGCCCAU | 8161 |
| Db | 8101 | GAAAGGTTTTGCGTGCATGATTTTCAACCAACCAATTT ATATGATCTTAATATGAATGGCCAT | 8160 |
| Qy | 8162 | GGACAGUCGGGAUGACUAAGUUUAUUGCGAUGGAUUA GUUUCUUAAGGUAACCUUCUG | 8221 |
| Db | 8161 | GGACAGTCGGGATGACTAAGTTTTATTTCGGATGGATGAT CTTCTAGGTAAACTCTCTG | 8220 |
| Qy | 8222 | AUGUUGGAUAUACCGCGAUGUCUGACGGAUUCA CGAUUUGACAGUUUCUUAACCAUACU | 8281 |
| Db | 8221 | ATGTTTGGATATACCGCGATGCTGACCGGATCA CGAATTTGACAGTTCTTCTTACACCATACT | 8280 |

| | | | |
|----|------|--|------|
| QY | 8282 | UGCUGAUAUGCAGUCUCGCGGAUUAAGGGAGUUUUUCAUGGAAGAUUGGGA CAUAGGCGUGC | 8341 |
| DB | 8281 | TGCTGAATTGCAGTGTCTCGGATTTAGGGAGTGTCTTTTCATGGAAGATTGGGA CATAGGCGTGC | 8340 |
| QY | 8342 | AGAUGCUUGGAAUUUCGACACUGAANAUAUUUACACCCCAUUGGCAACACCUAGUGGAA | 8401 |
| DB | 8341 | AGATGCTTTCGAAATTTTGCA CACTGAAATAATTTACACCCCA TTGCAACACCTGTATGGAA | 8400 |
| QY | 8402 | CAGUCGUCAAAAAGUUUCGAGGAAUAUAUGUGUGUCAACCGUCAACAGUCGUAUAACA | 8461 |
| DB | 8401 | CAGTCGTCAAAAGTTTCGAGGAATAATYATAGTGGTCAACCGTCAACGTCTGTAGATAACA | 8460 |
| QY | 8462 | CAUUGAGGUCUGUAUUUGUGCGAUUAAGUUUAUAUUGAAUAGUGUAAAAGUUUGAGA | 8521 |
| DB | 8461 | CATTGATGGTCTGTATTGTGTGTCAGTATAGTTTAAATTA TGAATAGTGTAAAGTTTGAGA | 8520 |
| QY | 8522 | AUCAGGAUGAUGUCGACAGUAUUUCGUUAACCGUGAUGAUUAUUCUUGCACAUAUC | 8581 |
| DB | 8521 | ATCAGGATGATGTCTGCAGGTATTTTCGTTAACCGTGTATTTATTGCTTTGCAATCAATC | 8580 |
| QY | 8582 | CAAAUUUAUACACAUCUAGAUUUUUUAAAAGUUCAUUUGUUAUUUAGGUUUUAGACU | 8641 |
| DB | 8581 | CAAAATTTATACACATCTCTAGATCTTTTAAAGTTCA TTTTGTCTAATTTAGTTTAGCT | 8640 |
| QY | 8642 | ACGAUUCUCUACUCGACGAAAGACAAAAGGAGAACUUUGGUUUUAUGUCUCAAAAGGAG | 8701 |
| DB | 8641 | ACGATTTCTCTCATCGAACGAAAGACAAAGAGAACTTTGGTTTATGTCTCACAAAGGAG | 8700 |
| QY | 8702 | UUAAAUAUAUGACUAGUAUAUUCCAAGCUGGAGCCAGAGAGGUGUUGUCUCAUAUUCUUG | 8761 |
| DB | 8701 | TTAAATTTAAATGACATGTATTTTCCAAGCTGGAGCCAGAGAGGGTTGTCTCAATACTTG | 8760 |
| QY | 8762 | AGUGGGAUAGAAGUGUAAAAACAGAACACAGAUUAGAAAGCAUUGUGCGUUUGCAUGAUUG | 8821 |
| DB | 8761 | AGTGGGATAGAGTGTAAAAACAGAACACACAGATTAGNAGCGATTTGGCGCTTCATGATTG | 8820 |
| QY | 8822 | AAGCAUGGGGUUACCCUAGGUUAAUCCA GAAAUUUGAAAAUUUUAUGCUUGGGUUCUGG | 8881 |
| DB | 8821 | AAGCATGGGTTACCCCTAGGTTAATCCACGAAATTCGAAAATTTTATGCTTGGGTTCTCG | 8880 |
| QY | 8882 | AACAAGCACCAUAACAUAUCUGCAUCUGAGGAAAGGCACCAUAUAUUUCGGAACAG | 8941 |
| DB | 8881 | AACAAGCACCATACAAATCATCTCGCATCTCGAGGAAAGGCACCATACATTTTCGGAACAG | 8940 |
| QY | 8942 | CGUCUAAAAGAUUUAACAUGCGAAGAAAGUGUGUAUGAAUUAUGUCAUUAUUAUUAU | 9001 |
| DB | 8941 | CGCTCAAAAGACTTTACATGCGAAGAGAGTGTCTGATGAATCATGTCTATCTTAG | 9000 |
| QY | 9002 | AGAUGUGUCAUGUAUUUGAACGAGUAGUA CUUUGAUGAUGAAGAUUGUUCUACAC | 9061 |
| DB | 9001 | AGATGTGTGCAAGTGAATTTGAA CGAGGATCAGTACTTTTGATGATGAAGATGTTTCTCACC | 9060 |
| QY | 9062 | AGUCCGCUUUGAUGUGGCAAAACCCACACAGACAGAAACAAAGAACGCAUGAAGAGAA | 9121 |
| DB | 9061 | AGTCCGCTCTTGATGTCTGGCAAAACCCACACAGACAAACAAAGAAAGCATGTGAAGAGAA | 9120 |
| QY | 9122 | AGAAUAAAGAGAAAAACGAGAAAAUAAAAACAAAAUAAAGAAAGUCGAGAGAAACAUG | 9181 |
| DB | 9121 | AGAAUAAAGAGAAUAAACAGAAAAATAAAACAAAAATAAAGAAAGTCGAGAGAGAAACATG | 9180 |
| QY | 9182 | AGAAAAUUCGAAUAGCGCAUCUGGUGCUAUGUUUCAAACAA CGAAAAAGACAAGGAUG | 9241 |
| DB | 9181 | AGAAAACTTCGAATAGCGCATCTGGTGCTATTGTTTCAAAACAACGAAAAAGACAAGGATG | 9240 |
| QY | 9242 | UCGAUGAUGAUAUGUGGAUCUUUAUCAUA CCA CGAAUUAUAUUCGAUAUCCAUAAC | 9301 |
| DB | 9241 | TCGATGTAGGATCAAGTGGATCTTTTCATCATCA CCA CGAATTTAATCGATATCCAATTAAC | 9300 |
| QY | 9302 | UCAUAUGCCAAAGUCGAAAGGGAAGAAUUUUAUUAUUGGAGUUCUUUAUCAAUAAC | 9361 |
| DB | 9301 | TCAATGTCCAAAGATGAAAGGGAAGGAATTTTAAATTTTGGAGTGTCTTTTTACAATACA | 9360 |
| QY | 9362 | CACCAGAUCAAGUGGACAUUUCAAAUACCA GGGGCAAGUAUUUCAUGUUUAUACAUGGU | 9421 |

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|----|------|-----|-----|------|------|--------|------|------|------|------|------|------|------|-------|------|-------|------|-------|------|------|------|------|
| Qy | 782 | GAC | AUG | CAAG | GCAC | UAGAAU | CGAG | CUAG | CAG | CAG | CAAG | UUGU | AGAG | GGAC | CAAC | AUC | CGGA | AGCAU | 841 | | | |
| Db | | | | | | | | | | | | | | | | | | | | | | |
| Qy | 782 | GAC | ATG | CAAG | GCAT | AGAAAT | CGAG | CTAG | CAG | CAAG | TGTA | AGAG | GAG | CAAT | CGGA | AGCAT | 841 | | | | | |
| Db | | | | | | | | | | | | | | | | | | | | | | |
| Qy | 842 | UAG | CAG | CGU | U | CGAAU | CU | CU | CAAC | U | CAAC | U | CAC | AG | AG | CAG | AGAA | CGG | 901 | | | |
| Db | | | | | | | | | | | | | | | | | | | | | | |
| Qy | 842 | TAG | CAG | CGT | T | CGAAT | CT | CTT | CAAT | CAAA | CT | CA | CAG | AG | AG | CAG | ATAT | AGAA | CGG | 901 | | |
| Db | | | | | | | | | | | | | | | | | | | | | | |
| Qy | 902 | UCU | UAA | CCAU | UCG | AAAU | UGG | AU | CAC | AG | CGU | GUU | UGAA | CCAAA | UAG | GAU | UUA | AA | 961 | | | |
| Db | | | | | | | | | | | | | | | | | | | | | | |
| Qy | 902 | TC | T | TAA | CCAT | T | CGAA | T | T | GG | AT | CAC | AG | CT | G | T | T | GA | CCAA | TAG | 961 | |
| Db | | | | | | | | | | | | | | | | | | | | | | |
| Qy | 962 | ACG | CAG | CU | AG | CGG | AG | GAAG | AG | AG | CU | AA | CAAG | AAAA | UCC | GUU | UGU | CA | CGU | 901 | | |
| Db | | | | | | | | | | | | | | | | | | | | | | |
| Qy | 962 | ACG | CAG | CT | AG | CGG | AG | GAAG | AG | AG | CT | AA | CAAG | AAAA | TCC | CGT | T | T | GA | CGG | 901 | |
| Db | | | | | | | | | | | | | | | | | | | | | | |
| Qy | 1022 | ACG | UCG | CGC | CGA | UA | AAAA | CU | CAU | GA | CCU | AA | CGU | CA | AAAG | AGG | AG | AG | AAAA | AGU | 1081 | |
| Db | | | | | | | | | | | | | | | | | | | | | | |
| Qy | 1022 | ACG | T | CG | CGG | AT | AGAA | CT | CA | TG | AA | CT | AA | CGT | CA | AAAG | AG | AG | AG | AAAA | 1081 | |
| Db | | | | | | | | | | | | | | | | | | | | | | |
| Qy | 1082 | AAG | CAA | CUG | A | CAU | CA | UUA | UAA | AG | CAG | CG | CA | AAUG | AAAA | AG | AG | AG | AG | AAAA | 1141 | |
| Db | | | | | | | | | | | | | | | | | | | | | | |
| Qy | 1082 | AAG | CAA | CT | GA | CA | CA | TAC | A | CA | TAC | AT | AA | AG | AG | CAG | CG | CA | TAT | AAAA | 1141 | |
| Db | | | | | | | | | | | | | | | | | | | | | | |
| Qy | 1142 | AAA | AUG | U | CU | CUU | U | GU | U | GU | U | GU | U | GU | U | GU | U | GU | U | GU | 1201 | |
| Db | | | | | | | | | | | | | | | | | | | | | | |
| Qy | 1142 | AAA | AT | G | T | G | T | CT | T | AG | T | AT | G | G | C | G | C | CA | T | AA | T | 1201 |
| Db | | | | | | | | | | | | | | | | | | | | | | |
| Qy | 1202 | GCC | AAA | AG | AU | U | CA | AG | AG | CU | U | GU | U | U | AU | CG | CA | AG | AG | AG | 1261 | |
| Db | | | | | | | | | | | | | | | | | | | | | | |
| Qy | 1202 | GCC | AAA | AG | AT | T | CA | AG | AG | CT | T | G | AT | T | CG | CA | AG | AG | AG | AG | 1261 | |
| Db | | | | | | | | | | | | | | | | | | | | | | |
| Qy | 1262 | GU | A | C | U | A | A | A | A | A | U | U | G | G | U | U | C | A | CU | U | A | 1321 |
| Db | | | | | | | | | | | | | | | | | | | | | | |
| Qy | 1262 | G | T | A | C | T | A | A | A | A | A | A | T | T | G | T | T | C | A | G | T | 1321 |
| Db | | | | | | | | | | | | | | | | | | | | | | |
| Qy | 1322 | A | A | G | A | U | C | U | U | G | G | A | U | C | U | A | U | C | A | U | U | 1381 |
| Db | | | | | | | | | | | | | | | | | | | | | | |
| Qy | 1322 | A | A | G | A | T | T | G | T | T | G | G | A | T | T | T | T | T | G | A | A | 1381 |
| Db | | | | | | | | | | | | | | | | | | | | | | |
| Qy | 1382 | A | G | A | U | A | A | A | U | C | A | A | U | A | U | C | U | G | A | G | G | 1441 |
| Db | | | | | | | | | | | | | | | | | | | | | | |
| Qy | 1382 | A | G | A | T | A | A | A | A | T | T | C | T | G | T | G | A | G | A | G | G | 1441 |
| Db | | | | | | | | | | | | | | | | | | | | | | |
| Qy | 1442 | A | A | U | A | G | A | U | A | G | U | U | U | A | G | U | A | U | A | U | A | 1501 |
| Db | | | | | | | | | | | | | | | | | | | | | | |
| Qy | 1442 | A | A | T | A | T | A | A | T | A | G | T | T | G | A | G | T | T | G | A | A | 1501 |
| Db | | | | | | | | | | | | | | | | | | | | | | |
| Qy | 1502 | G | U | A | C | U | G | A | U | G | C | C | U | U | C | A | A | A | U | C | A | 1561 |
| Db | | | | | | | | | | | | | | | | | | | | | | |
| Qy | 1502 | G | T | A | C | T | G | A | T | T | A | T | T | G | A | C | T | C | T | T | 1561 | |
| Db | | | | | | | | | | | | | | | | | | | | | | |
| Qy | 1562 | A | C | U | A | G | C | C | A | U | A | G | C | C | U | U | U | U | U | U | 1621 | |
| Db | | | | | | | | | | | | | | | | | | | | | | |
| Qy | 1562 | A | C | A | T | G | C | C | A | T | A | G | T | G | A | G | T | T | T | G | A | 1621 |
| Db | | | | | | | | | | | | | | | | | | | | | | |
| Qy | 1622 | U | G | A | C | U | U | G | A | U | A | G | C | C | U | A | G | A | G | C | C | 1681 |
| Db | | | | | | | | | | | | | | | | | | | | | | |
| Qy | 1622 | T | T | G | A | T | T | G | A | T | T | G | A | T | T | G | A | T | T | G | A | 1681 |
| Db | | | | | | | | | | | | | | | | | | | | | | |
| Qy | 1682 | A | G | U | G | C | G | A | A | U | G | C | C | A | A | U | U | C | C | A | 1741 | |
| Db | | | | | | | | | | | | | | | | | | | | | | |
| Qy | 1682 | A | G | T | G | C | G | A | A | T | T | G | A | A | T | T | T | T | T | T | 1741 | |
| Db | | | | | | | | | | | | | | | | | | | | | | |

| | | | |
|----|------|---|------|
| Qy | 1862 | UGGAUCAUUUUUUAUUCGAAUUGAGAAUAGUCUGAUAUCGGAUAGAACACAAAACUUCGAUG | 1921 |
| Db | 1862 | TGGATCAATTTCTTAAATCGGATATAGAAATAGTCTGTAATCGGATGGAACACAAAATTTCGATG | 1921 |
| Qy | 1922 | CGCACAACAAAUUUGCACAUAUUNUUGGCAGUCGCCAAGAGAUAUCCUUUUUCAAUUUAG | 1981 |
| Db | 1922 | CGCACAACAAAUUUGCACAUAUUNUUGGCAGUCGCCAAGAGAUAUCCUUUUUCAAUUUAG | 1981 |
| Qy | 1982 | AGCAUCUGAAUUGCUAAUUAAGUCGGAUAAAACUUGUUAAGCGAGGAUUUUUUAUGAAA | 2041 |
| Db | 1982 | AGCATCTGAATGAATTCGTAAATTAATGGCAGTCGCAAAAGAGATTTCTTTTCCAATTTTAG | 2041 |
| Qy | 2042 | UGUCUCAAUUGCCUUUUAAGACUACACGCGUGGCAUAAAAACAGAGCGAUUUAUUAUUAAGA | 2101 |
| Db | 2042 | TGTCTCAATGCCCTTTTAAAGACTAAACGCTGGCATATAAAAACAGGAGCGATTCATTCAGA | 2101 |
| Qy | 2102 | AGGAGAGAUUCCCAUUCUCCGAAUUAAGAUGUACAGUAAGCAACAUAUUAUUUUGCAU | 2161 |
| Db | 2102 | AGGAGAGATTTACCATTTCGGAATTAAGATGTGAGTAAAGCACAAATTTAAATTTTGTCAT | 2161 |
| Qy | 2162 | UGAUGUGUGACAAACCAACUUGACAAAAUUGGUAAACUUCUGUGUGGGUGAAAGAGGUUAUC | 2221 |
| Db | 2162 | TGATGTGTGAACCAACTTGTGACAAAATGGTAACCTTCGTGTGGGTGAAGAAGGTTATC | 2221 |
| Qy | 2222 | AUGCGAAGAGGUUUUUCUAAAACUUCUUGAGAAAAGUUAUCAAACUGACGGUUUAUAGA | 2281 |
| Db | 2222 | ATCGAAGAGGTTTTTCTTAAACTTCTTTGAGAAAAGTTGATTCAAATGACGGTTATAAGA | 2281 |
| Qy | 2282 | AACACAUAUGCGAGUACAACCCAAAUUGGCHACAGACAACACAGCUAUUAGGNAACUGAUUU | 2341 |
| Db | 2282 | AACACATAATCGGAGTCAACCCAAATGGCCAACAAGACAAACAGCTATAGGAAAACTGATTT | 2341 |
| Qy | 2342 | UAUCGCGGAUCCAUCUACGCUACGACAAACAAUAGAAAGUAGCCCAUUCACAAAGAGUUC | 2401 |
| Db | 2342 | TATCGACGGATCCATCTACGCTACGACACAAATGAAGAGGTAGCCCCAATCACAAGAGTTC | 2401 |
| Qy | 2402 | CAGUUGGUAAAUAUUGUACAAGCAAAAGAGAUGGUUGUUAUCGCUUACUCCAGCAGUCUGUG | 2461 |
| Db | 2402 | CAGTTGCTAAATATTGTACAAAGCAAAAGAGATGSGTTGTACGTCATCCAGCATGCTGTG | 2461 |
| Qy | 2462 | UUAACAUGGAAGUUAUCGCCAUUGUUUUCUGAUUAUACAAGUAGCCCAACUAGAUAUUAUC | 2521 |
| Db | 2462 | TTACAATGGGAAGATGGTACGCCATGTGTTCTGATATCAAGATGGCCAACTTAAGAAATCATC | 2521 |
| Qy | 2522 | UAGUCAUUGGAAAUUCAGAGAGAUCCAAAGUAUUGUAGUAUACCAAGCAGCUCUCAAUGACA | 2581 |
| Db | 2522 | TAGTCATTGGAAAATTCAGGAGATCCAAAGTATGTGGATGTACCAGCAGCTCAAGTGACA | 2581 |
| Qy | 2582 | UGAUGUGGCUAAGGAAGUUUAUUGUUAUCUACAACAUUUUUGGCAAUUGUUGCUGAAUG | 2641 |
| Db | 2582 | TGATTGTGGCTAAGGAAGTTATTGTTATCTCAACATTTTTCTTGGCAAATGTTCTGCTGAATG | 2641 |
| Qy | 2642 | UGAAUGAGAGUGAAUCAAUAUUAUUAUACAAGAAAGUUUAGAGUAUUAUUGUACACCGGUC | 2701 |
| Db | 2642 | TGAATGAGAGTGAATCAAAATCAATTCACAAAGAGGTTAGAGATATAATTTGTACCGCGTC | 2701 |
| Qy | 2702 | UCGUGUCAAUGCCCAAGCUAAAUUCGAUUGUCCAAUGAAUUGUUAUCUUAUACAGCCUCC | 2761 |
| Db | 2702 | TCGGTCAATGGCCAAAGCTTAATCGATGTTGCAACTGAAATGTTACTTCTATCAGCCCTTC | 2761 |
| Qy | 2762 | ACCUGAAAACGAAAAUUGCUGAGUUGCCCCGAAUUCUUGAGGUAUUAUUAUUAUUAUUA | 2821 |
| Db | 2762 | ACCCTGAAAACGAAAAATGCTGAGTTGCCCGGAATTTCTAGTGGATCATACATCAAAATGTA | 2821 |
| Qy | 2822 | UGCAUGAUGAGUAUUAUUAUGGUCGCUAGACACGCAUUUUUUAUUGUUAUUAUUAUUAUUA | 2881 |
| Db | 2822 | TGCATGTATCGATTCATATGGCTCGCTAGACAGCAAATTTCTATGTTCTGAAAGCGCAATA | 2881 |
| Qy | 2882 | CUGUAUGCACGUAUUAUAUUCGCGAAUUAUGCAUUGAUUCGAGCUGCAAAACUAUUUU | 2941 |
| Db | 2882 | CTGTAAATCAGCTAAATTTAAATTTCCGCCGATTAATGACTTTGGATTCGGAGCTGAACATTAIT | 2941 |
| Qy | 2942 | UAGUAGUGGAGAGACCUCAUAGCAAGCAAGCUCUCCAGUGUUCUCAAUAAAUUAUCUGUA | 3001 |

| | | FEATURES | | Location/Qualifiers | |
|------------|-------|---|-------|--|--|
| | | source | | | |
| QY | 9542 | UGAUGCAAGGGGAGAACAAUACGUAUACCCCUUACCAACAAUAGUGGAAAACGCAAAAC | 9601 | 1..9798 | |
| Db | 9542 | TGATGCAAGGGGAAAGAAACAAATCGAATACCCCTTCAACCAATAGTGGAAAACGCAAAAC | 9601 | /organism="Turnip mosaic virus" | |
| | | | | /mol_type="genomic RNA" | |
| | | | | /isolate="A64" | |
| QY | 9602 | CCACUUGGUCAGAUUAGUGGUCACUUVAGCAAUUGUCUAGCAUGCAUACUGGAAAAGA | 9661 | /db_xref="taxon:12230" | |
| Db | 9602 | CNACTTTGGCTCAGATTATGGCTCACTTTAGCAATGTTGCTGAGCATACATCGAAAAGA | 9661 | <1..94 | |
| | | | | 95..9589 | |
| QY | 9662 | GAAAUUAGAGAGCCAUUAUAGCCGAGGUA CGGUUAUCAAACGGAACCUACCGACAUGA | 9721 | /codon_start=1 | |
| Db | 9662 | GAAATATGAGAAGCCATATATGCGGAGGTACGGTATTCAACCGAACCTCACCGACATGA | 9721 | /product="polyprotein" | |
| QY | 9722 | GUUGGCGGAUAGCUUUGAUUUAUGAAUAGCAUUAUGCAUACAGGACCGCAGUCGGGCC | 9781 | /protein_id="BAC79396.1" | |
| Db | 9722 | GTTTGGCGGATATGCTTTTGATTTCTATGAATGACATCAAGGACCGCAGCTCGGGCCC | 9781 | /db_xref="GI:33146225" | |
| QY | 9782 | GGGAAGCCACAUCCAGUAGAAAGCUGCAGCAUUGCAGAUUGCAGUAGCAUUAUAGAUGUUG | 9841 | /translation="MAAVIPASAITNATINKLTSTGMVQFGSPFPVPLRSTTAIVVT | |
| Db | 9782 | GGGAAGCCACATCCAGATGAAAGCTGCAGCATTGGGAGATGGAAATAATAGATGTTTG | 9841 | PVTQPKLTMQFSGSLDPIVVKGEAGSSVKETRRQLNVKEDVNLGATLAVLVVKQSSI | |
| QY | 9842 | GACUGAUGGAAAAGUCGGAUUGCGA CUGAGAACACGAGGCGCCACACCGCAGACGAG | 9901 | VVRQEEANRERAIPLDFENSILGRPYGTAKNEKVIIMTARGVKIPSTKTRAMKHRA | |
| Db | 9842 | GACTGGATGGAAGAGTCGGAATGCGACTGAGAACACGAGGCGCCACACCGCAGACGATG | 9901 | RERLRBQPIKTLKWEPLSEFISIGGSPAKTIEBEETHTKWPLTKTSTKTRVHKHKA | |
| QY | 9902 | UTUACCAUACACUCACUAGCAUICACCGCGUUGCAUUAUAGAUUAUUAUUAUUAUUAU | 9961 | KMDLQGIEMLRSLIKIPKAKNANIEFTDKKTIKVDFVRKERTFARIPQAVHLGKRG | |
| Db | 9902 | TTAACCACTAACACTCATCATTCATTCACCGCGTTTCGATATTATTAGATATTTTACCTA | 9961 | KRDLLSGEENQFIDILISSENGNTAKIPGVVACAGSIVVNRNBLITQKRSRSPQAF | |
| QY | 9962 | AGUUAUACUAGUACUUAUUAUACGCAUUGCUUACUUAUUGCAGCAGCGUUAUGAGG | 10021 | VIRGEHEGVALDMCLAIKVTRTMWHKIVHFSAAAGANFWKGFDRCFLAYRGSDEHYCTG | |
| Db | 9962 | AGTTTATCTAGTATCTTTTAAATCCCATAGCTTACTTCTTAGCACCGCTTAGTGAGG | 10021 | LDVTECGEVALMCLAIKVTCTPCDICTDSEL SQOASASSIRHRLVOLREVTKSS | |
| QY | 10022 | UUUUAACCUUUAUUAUGUCAGAGGAGGUAAGCGGUAAGCCUCUGUGAUCUCUUAAGAA | 10081 | YPRFHAVQIILDRYEQLSHGENANYQDFAEIQSLTDGMEKAAFPHANKLNAILLKAT | |
| Db | 10022 | TTTATCTCTATATCTATGTGTCACTGAGGTAGCCCTCGTGTGATCTCTTAGAAGT | 10081 | ATGBEYBOATKHLLEITRYMKRNTENIEKSLKFRNKISOKAHINPFLMCDNQLDN | |
| QY | 10082 | AUGUCCCAAGCUGCAGUGGUGGUUUAUAGCAUAGAGUGGUCUAGGACCUUAGCC | 10141 | GNFTVBGRGYHAKFFSNYFEIIDPKGYQTYETRI VPNGSRKLAIGKLIYPTNFEVL | |
| Db | 10082 | ATTGTCCTCAAGTGCAGTGGCTGGTTGTTTCATAGCATGATGAGTGAGCTTCAGCC | 10141 | REQMRGFPVESHPITVECVSKQSGDFHACCCVTTESGDPVLSDKMPTKHLVIGNS | |
| QY | 10142 | UAAGCAAGGAGGG 10154 | | GDPKYVDLPEIENKMWIATKRGYCVINIFLAMLVNVKESQAKFTKVVRDKLVBELGK | |
| Db | 10142 | TAAGCAAGGAGGG 10154 | | WPTLLDVATACYFLKVPYDVANAEALPRMLVDHKTCLIHVVDSSGLSTGYHILKNT | |
| RESULT 3 | | | | VEQLIKTRQNLESLSLGRYVGGTKWEDAHGASINIDPQWCIIRRLIKGVYRPKQKED | |
| AB093599 | | | | MLTNPFPLFALLSPGVIILAFYNSGLEIYLMNYIKADNSIVALLVLVLAKVASAS | |
| LOCUS | | | | QSVLAQQLVIERSLPELDEARANTVGPDSAAQACNFKLGLMLIHMSFPNNLASGGYT | |
| DEFINITION | | | | ILRHSITLQILEVLSLOILDEAWSELSSERCAIKYYSKQAI FQORDLPMSQSDLGG | |
| | | | | RYSRSVSSYSEWSQRMKKLYSGLCNKTRNSVSMWSGVSSVCCTINLYPVDVFKPI | |
| | | | | NVLVCISLITITASEANRIVTAQRKLDVADTERKLEIWELEAFHHSILTHSAKQHT | |
| | | | | FDEFVISAANAPHLSEHIEEKAAVHQARQSELELIRIVA FALVLMFMDAERSD | |
| | | | | CVTLINKLGLSVTEFTVYHQALNDIEDLTLERNLFVDFPELSDSISIVQOLPAEKT | |
| | | | | FASWMSHQLSRGFTI PHYRTGKEMTFTRATATEVAGRIAHSKDILLMGAVSGKS | |
| | | | | TGLPVHLSRKGNVLLRPTPLAENVHKQLSQAPFYQNTLMRGLTAFGSAPI SVMT | |
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| | | | | LLAERDFKVDKTDGTMKVGNIETITSTGPKRHFIVATNIIENGVLIDIDVDAFGT | |
| | | | | TEAALKCFYGLPVTINNVTSLILGNVTQOARTMSVEFETPFYTSQVVRVYDGMHPQ | |
| | | | | VHALLKRFKLRDSEVTLNKLAI PNKGVNAMLTA SEYARLGA NVANEDRDRVPPFMRDQI | |
| | | | | PEKLHLEMDVVVKFGDAGFRLSSASAKVAVTLOTVNSIQRTVTI IDTLTABER | |
| | | | | RKQSYFXTVTSNCVSSNFSLQSTNAIKSRMKDHTCENISVLEGAKSOLLEPRNL | |
| | | | | ADHSFTTKSDGISRSPMSDYGALAEVHQHSTNEMSKFLKAGKNRLLITRDVLVIGC | |
| | | | | VLGGVWMI IOHLSQGITEPVTHAKGRQKLRKFNARDTKMGREVIYGGDDTIEHY | |
| | | | | FGEAYTKGKSGKTRGLGHKRNFINNYGDFDPDSAVRFDPLTGTALDENPFTDI | |
| | | | | TLVQKHFGDIRDLLAQDELEPESIRFQKTIQAYVTNNKTGKALKVLDITLPHMLKVC | |
| | | | | NLHATAGPPEFEFLROTGAQPI SIDVPKANTEVSVSDHSSPMFGLRDNYPISN | |
| | | | | NICHLTNNSDGASNLVGVGPGPLITNRHLFEENGEILLIKSRHGFVIRNTTQLHL | |
| | | | | LPIDRDLILLIRLPKDI PPPQKLGFRQPEKGERICMVGSNFQTKSITSVYSESTVM | |
| | | | | PVENSQFQKHWISTQDQCGSPMVTSDKGLILGHLSLANFQNSINYFAFPDDFAERY | |
| | | | | LHTFETHEWHKHWKNTSGISWGLNT QAAQAGL FVKSLISDLSTAVTAQOQNR | |
| | | | | WNFQELGNLKAIAHCPSQLVTKHTVKGCMQFDLYKLHDEAREYFQPMLGQYQKSK | |
| | | | | LNREAYAKDILLYATPIEAGNIDCDLFEETVEI VISDLWNYGFVCVYTDI DIFEA | |
| | | | | LNMKSAYCALYKGGKDYFAEFTPEMKEILLKQSCERLFLGKMGVNGSLKAEARPLE | |
| | | | | KVEANKRTTFAEFLDILLGGKVCDDPNNOFYDHNKLKAPMSVGMTFYFCWDRLLQS | |
| | | | | LPDGMVYCDADGSGDSQSPYLINAVLINIRLEFEEEMWDIGEVMLRNLYITETPIS | |
| | | | | TPDGTLYVKKFKGNSSQSPSTVDNTLAVILAVNYSLLKSKGPSBELRDSIVFFVNGDD | |
| | | | | LLLSVHPREYELDTMADNFRGLKVT FDSRTKEKGLDMFMSQGHREGIWI PKLE | |
| | | | | PERTVSI LEWDRSKEPCHRL EAI CAAMIESWGYDRLTHEIRKFAWVTEQAPFNLSAQ | |
| | | | | EGKAPYAETALRKL YLDKESQSDLTQYLEAI PEDYEDGTVCVYHOANTLDLAGLT | |
| | | | | BEQQAOKERKERKTEKEREKQKAL KKGKGSQDQEDGRDKVNAKSTGTFSPVRL | |
| | | | | KSLSAOKMRVPKYEKKLLALNDHLILYTPETQDLSNTRSTQKQNFTEFGVWADVELTE | |
| | | | | DKMQI ILNGLMVCIENTSENIENMMMDQDQVEFPFKPLDHAKEPTFRQINAHF | |
| | | | | SDVAEYITEKNQDRPYMPRYGLQRLNTDMSLARYAFDFYEMTSTPTFRAREAHITQMK | |
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| | | |
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| 1202 | TGGAAGAGATTTCACAGATGCTTTCTTTCGGTACCTGGCGAG---TGATCGAGAGCACACG | 1256 |
| 1657 | UGCAAGGCCCAUAAACGUGUAGGAGUGUGGCGAAAUAGSCAGCCACCAUUGUAAACCAACUC | 1716 |
| 1259 | TGTTACACAGGACTTGACGGCTCACTGAAATCGGAGAGTAGCAGCTTTAAATGTGCCTTGCC | 1318 |
| 1717 | CUAUUCCAAUGGGAUAAUAACAUGCAUCUACAUGGAGGAGAACUGCUAGAAUUGUUGUCA | 1776 |
| 1319 | ATAATTTCTTGTGGCAAAATAACTTGTTCGGCACTGCATTACCGACAGTGAATTTATCACAA | 1378 |
| 1777 | CAAGAAGAGGAACUUGAAUUCUUCAGCGGCUAAAGAGGCCAAUUGGCGAAGUAAAUUAUCC | 1836 |
| 1379 | GGCCAGCAGTCGATCCAGTATTAAGGCACAGATTAGTTCNAITGAGGGAGGTTATTAAAG | 1438 |
| 1837 | AGUCUUCAUCAUAAAUUUCUUAACGUGGUAUCAUUUUCUUAUACGUAUGAGAAUAGUCUG | 1896 |
| 1439 | TCGAGCTATCCACGATTCAAACATGCAGTACAGATATTAGTAGGTATGAGCAATCACTT | 1498 |
| 1897 | AUUCGGUAGNACAACAACUUCGAGUGGCCACAAACAUAUUGCACAAUAUUGGCAGUCGC | 1956 |
| 1499 | CACGGTGAACAACCGCAACTATCATGAGTATTGTCAGAGATCCAAAGCCCTGCACCGATGGAATG | 1558 |
| 1957 | AAAGAGAUUCCUUUUCUAAAUUAGAGCAUCUCGAAUGAAUUGCUAAUUAUAGUCGGAUAAA | 2016 |
| 1559 | GAANAAGCAGCATTCGCCACATGCACAAACAGTTGAAATGCCATATCTAATCAAAGGGGCACG | 1618 |
| 2017 | CUUUGAGCGAGAUUUCUAUGAAUUGUCUCAAUUGCCUUUUGAGAGCUAACACCGUCGCAU | 2076 |
| 1619 | GCAACAGGTGAAGAGTATGAACAAGCAACGAAACACTTGTCTAGAAATCACCCGGTACATG | 1678 |
| 2077 | AAAAACAGGAGCGAUUCAUACAAGAGGAGAGAUUCAUUAUUGCAUUAUAGAUUGUCA | 2136 |
| 1679 | AAGAAATCGCTAGAGAAATATTGGAAGAGGGATCACTAAAAATCTTTTGAATAAAGATATCT | 1738 |
| 2137 | GGUAAAGGACAAUUAUUAUUGCAUUAUGUUGUGACAAACCAACUUGACAAAAAUGGUUAC | 2196 |
| 1739 | CAAAAGGCACAAATTAATCCCAACATTGATGTGTGTAATCACTCGACAGAATGGCAAT | 1798 |
| 2197 | UUCGUGUGGGUAGAAAGAGGUUAUCAUGCGAAGAGGUUUUUCUUAACUUUCUUGAGAAA | 2256 |
| 1799 | TTCAATGGGTGAAGAGGTTATCAGCAAAAGAACTTTCAGCAATTACTTTGAGATA | 1858 |
| 2257 | GUUGAUUACAUCGACGGUUAUAGAAACAACAUAUUGGAGUACAACCAUUGGCACNAGA | 2316 |
| 1859 | ATTGATCCAAAGAGGGCTACACTCAGTAGCAGACACGAAATAGTGGCCAAATGGCTCCAGA | 1918 |
| 2317 | CAACACGUUAUGGAAAAUCUGAUUUUAUUGCAGCGAUCCAUUCGCUACGCAACAUAUG | 2376 |
| 1919 | AAACTTGTCTATTGGCAGCTCATAGTTTCCAAACAATCTTCGAGGTCTTGAGGAGCAANTG | 1978 |
| 2377 | AAAGUAGCCCAUACAAGAGUUCUAGUUGGUAAAUUUGUACAAGCAAAAGAGAUUGU | 2436 |
| 1979 | AGAGGAAACCTGTGGAAATCGCATCCAATCACCGTAGAGTGTGTAAGTAAGTCACAAGGT | 2038 |
| 2437 | UGUUAUGCUUAUCCAGCAGUCUGUUAUCAAUGGAGAGUGGUAGCCAUUGUUUUCUGAU | 2496 |
| 2039 | GATTTTGTTCATGCGTGTCTTTCGCTCACCAACGAAATCAGTGTATCCAGTCTTATCAGAT | 2098 |
| 2497 | AUCAGUUGCCAAUAGRAUCAUUAUUGGAAAAUUCAGSAGAUUCCAAAGUAUUGUG | 2556 |
| 2099 | ATCAAGATGCCAATTAACATCACTCGTTAATTTGGAATAATGCGCGGATCCGAANTATGTC | 2158 |
| 2557 | GAUGUACCAAGCAGCUCA---AGUGACAUGAUUUGUGCUAAGGAAGGUUAUUGUUAUUCU | 2613 |
| 2159 | GACCTCCAGAAATCGAAGAGAACAAAATGTCATAGCCCAAGGGGTTATTGTTACATT | 2218 |
| 2614 | AACAUUUUCGCAUUGUUGCUAAUGUGAAUUGAGAGUGAAUCAAUUAUUCUACAAG | 2673 |
| 2219 | AACATATTTCTCGCAATGCTAGTGAATGTCAAGGAATTCAAAGCGAAGGAGTTTCAACAA | 2278 |
| 2674 | AAGGUUAGAUUAUUAUGUACCGCGUUCUGUUAUGGCCAAGCCUUAUUCGUAUUGCA | 2733 |
| 2279 | GTTGTTAGACAAACTGCTCGCGAGTTAGTGAAGTGGCCCACTTTATGGAAGCTTGCA | 2338 |

| | | | |
|----|------|--|------|
| Db | 4494 | GAAGCAATTTGGCATGTGATTTTCGAAAGGAGACAATATCCTTTGTGTACGTGGCTAGTTATATA | 4553 |
| Qy | 4925 | AUGAGGUUGAUCAGCUCUCUAAAAAUGUCGCGAGAAAGGCUAUUUUAGUGACUAAAGUCG | 4984 |
| Db | 4554 | ATGAAGTGGACACACTTTTCAAACTTCTGGCTGAAAGGACTTTAAAGTCACAAAGTCG | 4613 |
| Qy | 4985 | AUGGGCGUACACUGAAAAUUGGUUGACCGACAUAUUAUUAUAAAGGGAGUAGCCAGAAGA | 5044 |
| Db | 4614 | ACGGAAGAACAAATGAAGGTTTCGAAATATTGAAATTTACAACAAGTGGGACACCTAGCAAGA | 4673 |
| Qy | 5045 | AACAUUUAUUGAUCAGCAACCAACAAUAGCGAAGUAGGUGUACUCUACUAUGAUGAUGUUG | 5104 |
| Db | 4674 | AGCATTTTCATAGTAGCCACCAACATAATTGAAATTTGGAAATGGAGTCACACTAGATATCGACGTAG | 4733 |
| Qy | 5105 | UUGUGGACUUUGGUUUUAGAAAGUCACUGCUGAAAAUUGUAUUAUCGACAAACCGGUGCGUUAUUT | 5164 |
| Db | 4734 | TTGCTGATTTTCGGAACGNAAGTACTCCATACCTCGACACGGACAATAGGATGCTTAGCA | 4793 |
| Qy | 5165 | ACACAAAGACAGCAUUCUUAUCGAGAAACGCAUACAAAGAUUGGGCAGGUGUUGUAGAC | 5224 |
| Db | 4794 | CAACAAAAACAAGCATTAAATTATGGGGAGCGAATCCAAAGGCTAGGTAGAGTTGGTAGGC | 4853 |
| Qy | 5225 | ACAGAAGGGCAUGCAUAGAAUUGGAACUACAUIUAAAGUAUGAUGAUGAUAUCCUA | 5284 |
| Db | 4854 | ACAAACAGGCTACGCTCTCGGAATTTGGCCACACAGAAAAAGSTTTTGAGTGAAGTTCCAA | 4913 |
| Qy | 5285 | GUCUUGUGGCGACACAGCGUCUAUUCAAUGCUUACAUAUGUAUGAUGCCUGUAUAGACAC | 5344 |
| Db | 4914 | GTTTCATTGCAACAGAGCTGCTCTTAAATGCTTCAATATGAGTCTCCAGTGNATTACCA | 4973 |
| Qy | 5345 | AAGGAGUUUCAGUUUACAAGUUUACAAUUGCAUGCAGUCGACGCGCAGAGUAUUGUCUC | 5404 |
| Db | 4974 | ATAACGTTTTCACAAGTATTCTTGGTAAACGTTACAGTGAAGCAAGCACGACCATGTGAC | 5033 |
| Qy | 5405 | GUUUUGAUGUUGCGCUUUAUUUUGGCUUACAUUUAUUAUUAUGAUGGAGCAUGGACAC | 5464 |
| Db | 5034 | TGTTTCGAGATCACGCCATTTTACACAAGCCAGTAGTAGATACGATGSGATCAATGCAACC | 5093 |
| Qy | 5465 | CUGAAAAUUCACAAGCAUUAUUCUUAACAGUUUAGUAUGAUCUGAAAUUUAUUAUUGAUG | 5524 |
| Db | 5094 | CACAAAGTGACGCACTCTTGAGAGATTCAAGCTCAGGGATTTCTGAAGTTACACTAAACA | 5153 |
| Qy | 5525 | CCAUGGCUUUUAAACUUUACCGUAAACAUUUAUUGGCUAGAUUGUAAAUUUUUAUGACAGUA | 5584 |
| Db | 5154 | AGTTAGCCATACCAACCGAGGAGTGAATGCTTGGCTCACAGCTAGTAGTACGCTCGAC | 5213 |
| Qy | 5585 | UAGAAUCCCAUCUUGAUUUUCCGCGCGAGCAAAAUUCCAUUCCAUUUGUAGAGAAUUC | 5644 |
| Db | 5214 | TTGCGCGAAATGTTTGAGGACAGGCGCGATGTGAGAAATCCCTTTTCATGTCGTGACATTC | 5273 |
| Qy | 5645 | CAGAAUUGAAUACCGACACUUGUGGAGAGUAUUCUCAAUUAUUAAGACCAUAAAUUUGU | 5704 |
| Db | 5274 | CAGAAAACTCCATCTAGAAATTTGGGATGTGTTGTTTAAATTTCAAAGGCGACGCGGCT | 5333 |
| Qy | 5705 | UUGUAAGAAUGAGUUGUUGAGCCCAACAAAAGUAGCAUAUACAUUAAACACAGACAUUC | 5764 |
| Db | 5334 | TTGGCGCTCTCTCAAGCGCAAGTCAGCAAAAGTAGCTTACACATTGCCAAACAGATGCTCA | 5393 |
| Qy | 5765 | AUUCAAUUGGAAAAUUCUCUGGAUAUAUUGACGCGCCUUGUUGCAAGAAUAUUAAGAAAC | 5824 |
| Db | 5394 | ACTCCATTCAACGAACAGTCACTATCATAGACACATTAAATCGCTGGAAGAGAGAAGAAAGC | 5453 |
| Qy | 5825 | AGCAUUAUUUAAAGCAUAGCAAGUAACGCAUUGAUGUGGGAACACUUUUAUUGCUAA | 5884 |
| Db | 5454 | AAGAATACTTCAAGACAGTGCATCTAATTTGCGTTCCTTCTTTCGAATTTTTCCTACTACA | 5513 |
| Qy | 5885 | GCAUAGCAAAUGCAUACGGAACCAACUAUUGCUAAGGACUACACUGGCGCAUAUUAUCAGA | 5944 |
| Db | 5514 | GCATCAAAATGCATTAAGTCTCGTATGATGAAGACCAACACATGTGAAAAACATATCAC | 5573 |
| Qy | 5945 | AAUUCAGGCGCAAGAAUAUUAUUGGAAUUUCGUCAAUUUAAAUUUAUUGAUUCCUCCG | 6004 |

[illegible]

QY 7043 UCCACCCUUUGCAGAGGUUACGUAUUAAGAAUCCAAUAGUGGUGUAUUAUUUGUC 7102
Db 6714 TCCACCTTTTCCCAAAATTTGGGTTTCAGACACCTTGAGAAAGGGGAGAGATTTGTA 6773
QY 7103 UUGUUGAAUAAGUUUCCAAAGAAAGUAUUAUUGCAAGCAUUGUUUGAGAGCAAGCAAAA 7162
Db 6774 TGGTGGATCTAATTTCCAGACGAGAGCATTTACTAGCGTGTCTCAGAGACTAGCACAG 6833
QY 7163 CAUUCGCCAGGUGUAGAGGUUUAUUUGAAACAUAUUGGAUUAUAUCAAACGGAAGACAUU 7222
Db 6834 TTATGCCAGTGAGAAACAGTCAATTTTGGAAACACTGGATCAGTACTAAAGATGCTCAAT 6893
QY 7223 GUUGAUGCCUUUAUUAUGUUAUGUUAUGUUAUUAUUAUUAUUAUUAUUAUUAUUA 7282
Db 6894 GCGGTAGCCCAATGTTGAGCAAGAAAGGACGGAAGATACTTGGCTGTCATAGTCCCA 6953
QY 7283 GUCAUAAGUACGAUUAUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 7342
Db 6954 ATTTTCAAACTCCATCACTATTTTCGTCCTTTCCAGATGACTTGCAGCAAAATATC 7013
QY 7343 UUAACAAGUUAGAGAAACUGAAUUGGAGCAAAUUGGACUUAACAAGUUUAUAUUAUUA 7402
Db 7014 TCCACACATTTGAGAGCGCATGAATGGTCAAAACACTGGAAGTACAAACACTAGCGGGATCA 7073
QY 7403 GUUGGGCAACGAUAAACUUCAGGAUUGUUCUUAUGCAAGCAAGAAUUAUUAUUAUUA 7462
Db 7074 GTTGGGGCTCTCTAAACATTTCAAGCAGCACACCCAGCAGGTTTATTTCAAGTGAGCAAC 7133
QY 7463 UGAUUAAGCAGUUUAUGCAGCGAACCUUGUGUGCGCUCAGAGUAGCAUUAUUAUUAU 7522
Db 7134 TAATATCAGATCTCGACAGTACAGCAGTTTATGCA---AACACAGCAAAATCGATGA 7190
QY 7523 UUAUUAUACAGCTUGAAGAAUUAUUAAGCGGUGCAUUAUUAUUAUUAUUAUUAUUA 7582
Db 7191 TGTTCGAACAGCTCACTGGGAACCTTGAAGCAATTTGCACTTGCCTCAAGTCACTAGTAA 7250
QY 7583 CAAAGCAUUAUGAAGACAGUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 7642
Db 7251 CGAAACACACAGCTCAAGGAAGAGTGCCAAATGTTTGATTTTGACCTCAAAATACATGATG 7310
QY 7643 AAGCGAAUAGUUUUUUAACACAGUAGGGUUUUAUUGGGAAGAGCGGUCUUAACAAG 7702
Db 7311 AAGCAGAGAACTTTTACGCCAATGCTAGGCGAGTATCAGAAGAGCAAACTCAACCGAG 7370
QY 7703 AAGCAUUAUAAGGACCUUAUUAUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 7762
Db 7371 AGGCTTATGCAAGGATCTTCTCAAAATACGCGACACCAATCGAAGCAGGAAATATTGATT 7430
QY 7763 CUGAGAGUUUAAGUAGUUGGCGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 7822
Db 7431 GTGATTTGTCAGGAGAGACAGTTGAAATAGTCACTCAGATCTGTGGAATTTATGTTTG 7490
QY 7823 GGGAAUGCAAGUAUAUACCGAUUGUGACAGAUUUUAUUAUUAUUAUUAUUAUUAUUA 7882
Db 7491 AGGTATGCAACTACGTCACCGATGAAATCGATATATTTCGAAGCTTTGAATATGAATCTG 7550
QY 7883 CAGUGCGGCGUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 7942
Db 7551 CAGTGGGCGGTTATACAAAGGCAAGAGAAAGATTACTTTGCTGAAATTCACACCTGAGA 7610
QY 7943 AUCGAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 8002
Db 7611 TGAAGAGGAAATACTTAAACAAAGTTGTGAACAGCTTTTCTTGGGGAATTTGGGATTT 7670
QY 8003 GGAUUGGAAGUCUUAAGCUGAAUUAAGACCAUUAUUAUUAUUAUUAUUAUUAUUAUUA 8062
Db 7671 GGAACGGCTCACTTAAAGCAGAAATTCAGGCCACTAGAGAGGTGGAAGCGAACAACAC 7730
QY 8063 GAACAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 8122
Db 7731 GAACATTCAAGCAGCGCCATTTGGAACCTTTATTTAGGTGGAAGAAAGTTTGTGTTGATGACT 7790

QY 8123 UCAACAACCAAUUUUAUGAUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 8182
Db 7791 TTAAACAACAGTTTATGACCACAATCTTAAAGCCCCCTGGAGTGTGGATGACTAAGT 7850
QY 8183 UUUUUGCGGAGUAGAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 8242
Db 7851 TTTACTGCGGTGGATCGCTTGTGTACAATCACTGCCAGATGGCTGGATTTACTGCGATG 7910
QY 8243 CUGACGGAUACAGAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 8302
Db 7911 CAGATGGATCAAAATTTGATGTTTCACTATGCCATCTTATCAACGAGTACTCAACA 7970
QY 8303 UUAGGGAUUUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 8362
Db 7971 TCCGTTGAGTTCATGGAGGAATGGGACATAGGAGAGTCAATGTTGAGAAATCTGTACA 8030
QY 8363 CUGAAAUUAUUUAACCCCCCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 8422
Db 8031 CCGAGATAGTGTATACCCCTTATCAACACACAGATGGCACACTAGTGAAGAAATTCAAAG 8090
QY 8423 GAAUAUAUAGUGUUAACCGUUAACAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 8482
Db 8091 GAAATAATAGTGGACAGCCATCAACAGTCTGGGACACACACTTATGTCTACTAGCAG 8150
QY 8483 UGCAGUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 8542
Db 8151 TCAATTACTCTCAAAAGAGCGGTATACCAGTGAAGTGGCGGTATGTTGTAAT 8210
QY 8543 AUUCUGUUAACGGUGAUGAUUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 8602
Db 8211 TCTTTGTCAATGGCGAGTCTGCTGTTAGTGTTCACCCAGAAATATGAGTATGTTTAG 8270
QY 8603 AUUCUUUUAAGUUAUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 8662
Db 8271 ATACCATGGCAGCAAAATTCGTTGAACTGGGCTTGAAGTATATCTTTGACTCAAGAACAA 8330
QY 8663 AAGACAAAGAGAAACUUUGUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 8722
Db 8331 AAGAGAGGTTGATCTTTGTTTATGTCACACCAAGGTATAGAAGAGAGAAATTTGGA 8390
QY 8723 UUCCAAACUGGAGCGCAGAGAGGUGUUCUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 8782
Db 8391 TCCCTTAAATTTGGAACCAAGAAACGAATAGTGTGATTTTGGAAATGGGATCGGTGGAAGGAAC 8450
QY 8783 CAGAACAAGUUAAGAACGUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 8842
Db 8451 CATGCAATCGATTTGGAGCAATCTGCGCAGCAATGATCGAGTCAATGAGGTTATGACAGGT 8510
QY 8843 UAAUCCAGAAAUUCCGAAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 8902
Db 8511 TGACCCACGAGATAGCGCAAGTTTATGCGTGGTGAATTTGAACAGTCCATTCATCCT 8570
QY 8903 UGCACUUGAGGGAAAGGCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 8962
Db 8571 TAGCTCAAGAAAGGAAAGCCCTTACATAGCAGAAACAGCACTCAGAAAGCTTTACCTTG 8630
QY 8963 GCGAAGAGGAAGUUGCUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 9022
Db 8631 ATAAAGAAACCGTCAAGAGGATCTCACTCAGTACCTA----- 8668
QY 9023 ACGAGGAGUAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 9082
Db 8669 --GAAGCAATCTTTGAAGATTACGAAGATGGAAACGAAGTGTGCGTCTATCACCAAGCAA 8726
QY 9083 AACCCACAGCGAAACCAAGAAAGCAGUAGAGAGAGAAAGAAUUAUUAAGAAAGCAGG 9142
Db 8727 ATGAAACGCTAGTCTGCTGTTTGAAGAAGAGCAAAACAAGCAGAGAAAGAAAGG 8786
QY 9143 AAAUAUAAAACAAAUUAAGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 9202
Db 8787 AGAGAGAAACAGAAAGGAAACGAGAGAGCAAAAGCAGTTAGTCACTCAAGAAAGGCA 8846
QY 9203 CUGGUGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 9262

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| Qy | 7880 | CGGCAGUCUGGUGCGUUGUACAGUGGUUAGAAAAAGCGGUACUUCGAAAAAUUCCACAUUUG | 7939 |
| Db | 7502 | CTGCAGTGGGTGCAATTGTACGAGGGGAGAGAAAGATTACTTCAAGGATTTTATACACAAG | 7561 |
| Qy | 7940 | AUGAUCGAAAUCAUUAUUGCUACAGCUUAUGUGUCUCUCCGAUUAUUCUCAAAGGUGAUUUGGAA | 7999 |
| Db | 7562 | AGATGAAGGAAACAATTTTGGAAACAAGCTGTGTGACGGTGTGTACACAGGAAAAATGGTT | 7621 |
| Qy | 8000 | UUUGGAAUUGGAAGUCUUAAAAGCUGAAUUUAGACCAAUUUGAAAAGUUGAAGCAAAACAAA | 8059 |
| Db | 7622 | TATGGAATGGCTCTCTGAAAGCAAACTACGCCCCTTTAGAAAAAGGTTCAAGCCAAACAAA | 7681 |
| Qy | 8060 | CGCGAAACAUUACACAGCAGCUCCAUUGAAACAUUUAUUUGGCGGAAAGUUUGUGUGAUG | 8119 |
| Db | 7682 | CCCGCACTTTACAGCGCGCACTTGTATCATTTGCTGGGTGGAAAAAGCATGGGTGCGATG | 7741 |
| Qy | 8120 | AUUUCAAACAACAAUUUAUGAUCUUAAUAUGAAUUGCCCAUGGACAGUCGSGAUGACUA | 8179 |
| Db | 7742 | ATTTCAACACCAATTTTATGAGCTAAACATAAAGGGCCATGAGGTGTGGCATGACAA | 7801 |
| Qy | 8180 | AGUUUAUUGCGGAUGAAUGAUCUUCUAGGUAAACUUCUGAUGGUGUGAUUACCGCG | 8239 |
| Db | 7802 | AGTTTTACGGAGATGGAATGAACTTTTAAAGRAAGCTACCAGATGSGTGGATTCACTGTG | 7861 |
| Qy | 8240 | AUGCUGACGAUACAGAUUUGACAGUUCUCUUAACCAUAUUGUCUGAAUUGCUGUCUG | 8299 |
| Db | 7862 | ATGCGGATGGTTCACGTTTGTATAGTTCTTTTATCGCCTTATCTCATAAACGCACTCTTAA | 7921 |
| Qy | 8300 | GGAUUCGGAGUUUUAUCAGGAAUGAUGGACAUUGCGGACAUAGCGGUGCAGUCGUGAAAUUUGC | 8359 |
| Db | 7922 | ACATAAGATTACATTTTCATGAAACATGGGACATAGGGGAGCAATGCTCGGAAATTTAT | 7981 |
| Qy | 8360 | ACACUGAAAAUUUAACACCCCAUUGCAACACCGAUGGAAACAGUCGUCGCAAAAAGUUUC | 8419 |
| Db | 7982 | ACACAGAAATTGTGTACACCCCAATTGCAACACCCAGATGGAACAAATTTGTAAGAAATTTA | 8041 |
| Qy | 8420 | GAGGAAUAUAGUGGUCACCGGUCACAGUCGUAGUAUACCAUUAUGAUGUCUGUUAUU | 8479 |
| Db | 8042 | AAGGGAATNACAGTGGGCAACCGGTCAACTGTGCTGGGCAACACACTTATGGTGTATTAG | 8101 |
| Qy | 8480 | GUGUGCAGUAUGUUUAUUGAAUAGUUAAGUUUGAUAUCAGGAUGAUGUCUGCA | 8539 |
| Db | 8102 | CTCTCAATATTCCTTACTTAAGATCGAGTGGNAGCGGAAACACACAGCAAGTAATTA | 8161 |
| Qy | 8540 | GGUAUUCUGUAAACGGUGAUGAUUAUUGUCUGCAUCAUCAUCCAAAAUUUAUACAUCC | 8599 |
| Db | 8162 | AAATATTTTCGTCAATGGTGAACGATTTGCTGTATAGTATAGACCCAGCATACGAAGGCCTC | 8221 |
| Qy | 8600 | UAGAUUUUUUAAGUUCUAUUUUGCUAAUUUAGUUUAUAGUAUAGAUUUCUCUCAUGAA | 8659 |
| Db | 8222 | TCGCACAATTCGAGGGAAATTTCAAGGAACTTGGTCTCAAGTATGATTTTAACTCCAGAA | 8281 |
| Qy | 8660 | CGAAGACAAAGAGGAAACUUUGUUUAUGUCUCAAAAGGAGUUAAUUAUAAUAGACUGU | 8719 |
| Db | 8282 | CTAGAGACAGGGTGAATTTGGTTCATGTCCTCATCAAGGGAAAGAGTGGAGGACATAT | 8341 |
| Qy | 8720 | AUAUUCAAACGCGAGCCAGAGAGGGUUGUUCUCAAUAUUUGAGUGGGAUAGAAGUGUAA | 8779 |
| Db | 8342 | GGATCCCAAAACTGGAACAGGAGCAATTTGTCTCAATCTTGAATGGATCGATCAAAGG | 8401 |
| Qy | 8780 | AACCAAGAACACAGAUAGACGUAUUGCGUUCGUAUUGUAGCAUUGGUGUUAUCCCUA | 8839 |
| Db | 8402 | AACCAGGCAATAGAAATGGAGCAATTTGCGCTGCAATGTAGTAATCATGGGGTCAACAAG | 8461 |
| Qy | 8840 | GGUUAUCCACGAAAUUCGAAAAUUUAUUGUCUUGGGUUUCGGAACCAAGCAACUAUUC | 8899 |
| Db | 8462 | AGCTAACTCATCAGATACGGAGGTTCTATGCATGGCTTATTTGGNCAAGCTCCATATCTCG | 8521 |
| Qy | 8900 | AUUCUGCAUCUGGGGAAAGCCACCAUAUAUUUCGAAAAACAGCGCUCAAAAAGACUUUA | 8959 |
| Db | 8522 | GACTGGCAGAAATTTGGAAGAACACCGGTACATTTGCTGAAGTGCATCTCGCAAGTTGTACT | 8581 |

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| Qy | 8960 | CAUCCGGAAGAAAGUGUCUGAUGAAUAACUAGUCAUAUU---AGAGAUGUGUGCGCAAGUG | 9011 |
| Db | 8582 | TGGATAAAGATGCAGATTCAGAGTCCATTGAGGTTTATCTTAAGAGACAATATTTTGAAGATT | 8641 |
| Qy | 9017 | AUUUGAACGAGGAUGAGUACUUUGAUGAUGAAGAUUUUCUACACGAGUCGCUUUGAUG | 9076 |
| Db | 8642 | ACACTCCGAACGAGAGGATTTATTTGTATATCATCAAAGTGCGCAGCACGTTGGATG | 8701 |
| Qy | 9077 | CUGCAAAACCCACAGCAGAAAAACAAGAAAGACGAUGAAGAGAGAAAAGAAAGAAAGAAA | 9136 |
| Db | 8702 | CTGGAAACAGTGCTCCAAGTAAAGCAAGNAGCAAGAGCGCAAGCTCCACTCAAGSCA | 8761 |
| Qy | 9137 | AGCAGGAAAUAUAAAACAAAUAUAAGAAGUCGAGAAAGAAAACUAGAGAAAACUUUCGAUA | 9196 |
| Db | 8762 | TTGCGCCAAACAATGGAAGGCTTTGAAACCGGCCGATGACCACAACGGGCAAAAAGCAACAAC | 8821 |
| Qy | 9197 | GCGCAUCUGGCUUAUUUUUCAACAAACGAAAAACAGAGGAUGUGAUGAUGGAUCA | 9256 |
| Db | 8822 | AAACT-----GTCAATCAATCTAGAAAAAGATGTCAATGTTGGCACAG | 8863 |
| Qy | 9257 | GUGGAUCUUUCAUACCAACGAUAUUAUCGAUAUCCAAUAAACUACAAUUGCCCAAAAG | 9316 |
| Db | 8864 | TTGGTACTTTTCAGTGCCACGGTTAAAGGACTTCACAACAAAATGAGCATGCCTAGAG | 8923 |
| Qy | 9317 | UGAAGGGAAGAAUUUUAAUUUUGAGGUCCUUUUAUAUAACACACAGAUCAAGUGG | 9376 |
| Db | 8924 | TCAGAGGGAAGCAGCTATGAACTTAGACTCATTGTTGGTGTACAAACCCAGAGCAAGTTG | 8983 |
| Qy | 9377 | ACAUUCAAUACGAGGCAAGUAUUUCAAGUUUAUAUGGUAACAACGCUUGUGAAGG | 9436 |
| Db | 8984 | ACTTGGCTAACACAAGGGCTACAAAGGAAACAATTTTGACACATGSTATGATGGAGTTAAAC | 9043 |
| Qy | 9437 | AAUCCUAUGGUGUCUGAUGAAGAAUGGGAUAUAUUUGAUGAUAUAUUGUUUGU | 9496 |
| Db | 9044 | GAGATTACAGTGTGGATGACAGCTCAATGCAAAATAATCCTGAATGATGATGTTGGT | 9103 |
| Qy | 9497 | GUUAUGAAAUGGAAACAUCCUCAAACUAUAAUGGCAUGUGUUUAUGAUGCAAGGGAAG | 9556 |
| Db | 9104 | GCATTGAAATGSCACTTTCACCAACAATAATGGAATGTGGGTCTGATGGACGGAGAAG | 9163 |
| Qy | 9557 | AACAAUCGAAUACCCCUUUAACCAAUHUGUGAAAAACGCAAAACCCAUUGCGUCUGA | 9616 |
| Db | 9164 | AGCAATTGAATATCCGATAAAACCAATTAATAGATCACGCCAAACCCACATTTTCGACAG | 9223 |
| Qy | 9617 | UUAUGGCUCACUUAGCAUUGUCGAAGUAACGAAACUAUCGAAAGAGAAUAUAGAGAAGC | 9676 |
| Db | 9224 | TAATGGCTCATTTGAGTTATGTCGTGAAGCATATATTGAAAGAGAAATCAGGAAAAAG | 9283 |
| Qy | 9677 | CAUAUUGCCGAGUAUGUAUUAACACGGAACCCUACCGACGAUGAGUUUGGCGCAUAUG | 9736 |
| Db | 9284 | CGTACATGCCACGCTATGACTTCAGAGNAACCTGACAGACATGAGCTCGCTCGCTATG | 9343 |
| Qy | 9737 | CUUUUAUUUAUUAUAGACAUAUCAAGGACGCGAGUCGGGCCCGGGAAGCCCAUCC | 9796 |
| Db | 9344 | CGTTTTGATTTTACGAAGTAAACATCAAAACAACGAGAGCGCGCGAAGCTCATATCC | 9403 |
| Qy | 9797 | AGAUGAAAGCUGACAUUCGAGAUCCGAAUAUAUAAGAUUUUGAUGGAGGGAAG | 9856 |
| Db | 9404 | AAATGAAGCAGCAGCCCTTAGAGGTGTGCAAAACAAGTTGTTGGATTGGAACGGAATG | 9463 |
| Qy | 9857 | UCGGAAUUGGACUGAGAAACAGGAGCGCCACACCGCAGCAUGAUUUUACCAUACACUC | 9916 |
| Db | 9464 | TCAGCAATATGGAAGAAACAACGGAGAGACACACAGCTGAAGATGTGAACCCGCAATATGC | 9523 |
| Qy | 9917 | AUGCAUUTACCGGCUUCGAUAU---UAUUAGAUUAUUUACCUAAGCAUAUUUUUCUAG | 9973 |
| Db | 9524 | ACAGCCTCTCCGCGTGAAGGCTGTGAAGCTATGTAGGTAAATGATATTATTATGTAG | 9583 |
| Qy | 9974 | UAUCUU | 9979 |
| Db | 9584 | TATCCT | 9589 |

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| D _b | 7922 | ACATAAGATTACATTTTCATGTGAAACAATCGGGACATAGGGGACGAATCTCTCGGCAATTTAT | 7981 |
| Q _y | 8360 | ACACUGAAAAUUAUUUACACCCCAAUUGCAACACCUGAUGGAAACAGUCGUCAAAGAAAGUUC | 8419 |
| D _b | 7982 | ACACAGAATTGTGTACACCCCAATTTGCAACAACAGATGGAACAATTTGTAAGAAAATTTTA | 8041 |
| Q _y | 8420 | GAGGAAUAUAGUGUGUCAACCGGUCAACAGUCGUAGNAUAACACAUUGAUGUGUCUGUAUUU | 8479 |
| D _b | 8042 | AAGGGAATAACAGTGGGCAACCCGTCAACTCTCGTGGAACAACACACTTTATGTTGTTATTAG | 8101 |
| Q _y | 8480 | GUGUGCAGUAUAGUUUAUUAUGAAUAGUUAAGUUUGAAGAACUGGAGUAUGUGUGCA | 8539 |
| D _b | 8102 | CTCTCAAAATATTCCTTAAAGATGGAGTGGAGCGGGAANAACAACAACAAGTAATTA | 8161 |
| Q _y | 8540 | GGUAUUCUGUUAACGGUGAUGAUUUUUGCUUGCAUAUCCAUAUCCAUAUUUAUACAACAUC | 8599 |
| D _b | 8162 | AATATTTTCGTCAATGGTGCAGATTGCTGATTAGTATAGACCCAGCATACGAAGGCCCTTC | 8221 |
| Q _y | 8600 | UAGAUUCUUUUUAAAGUUUAUUUUGUUAUUUAGUUUAGACUAAGAUUCUCUACUACGAA | 8659 |
| D _b | 8222 | TCGACAACAATCGCAGGGGAAATTTCAAAGGAACTTGGTCTCAAGTATGATTTTTTAATCTCCAGAA | 8281 |
| Q _y | 8660 | CGAAGACAAAGGAGAACUTUUGUUUAUGUCUCACAAAGGAGUUAUAUUAAUUGACAUGU | 8719 |
| D _b | 8282 | CTAGAGACAAGGGTGAACTTTTGTGCCATGTCTCATCAAGGGAAAAGAGTGGAGGACATAT | 8341 |
| Q _y | 8720 | AUAUUCAAAGCUGGAGCCAGAGAGGGUUGUCUCAUAUUGAUGUGGAUAGAAUGUAA | 8779 |
| D _b | 8342 | GGATCCCANAACCTGGAACAGAGCGEATTTGCTCAATACTTTGAATGGATCGATCAAAGG | 8401 |
| Q _y | 8780 | AACAGAAACACAGUAUAGAACGUAUUUGCCUUCGAUGAUUUGAAGCAUGGGGUUAUCCCUA | 8839 |
| D _b | 8402 | AACCAGGCAATAGAAATGGAGGCAATTTGCGCTGCAATGATAGAAATCATGCGGGTCACCAAG | 8461 |
| Q _y | 8840 | GGUUUAUCCACGAAUUCGAAAUAUUUUAUGUCUUGGGUUCUGGACCAAGCACCAUACAUC | 8899 |
| D _b | 8462 | AGCTAACTCATACAGATACGGAGGTTCATGCAATGGCTTATTTGGACAAGCTCCCATCTCGG | 8521 |
| Q _y | 8900 | AUCUGCAUCUGAGGGGAAAGCCACCAUAUAUUUCGGAACACGCGCUCAAAGACUUUAUA | 8959 |
| D _b | 8522 | GACTGGCGAGAAATTGGNAAAGCACCGTACATCTGCTGAAAGTGCACTCCGCAAGTTGTACT | 8581 |
| Q _y | 8960 | CAUGCAGGAAGGAUGUGUGAUGAAUAUAUGUCAUUAUU---AGAGAUGUGUGCAAGUG | 9016 |
| D _b | 8582 | TGGATAAAGATCGAGATCAGAGTGCCATTGAGGTTTATCTAAGAGCAATATTTGAAAGATT | 8641 |
| Q _y | 9017 | AUUUGACAGGGAUGAGUAUUUUGAUGAAGAUUUUCUACCAAGUCGCUUGAUG | 9076 |
| D _b | 8642 | ACACTACCGAACACAGAGGATTTATTTGTATATCATCAAGTGGCGACGACACGTTGGATG | 8701 |
| Q _y | 9077 | CUGSCAAACCCACAGCAGAAACAAAGAAAGACGAUGAAGAGAGAAAGAAUAAAGAAAGAAA | 9136 |
| D _b | 8702 | CTGGAACAGTGTCTCAAGTTAAGCAAGGACGAGAAAGCGCAGCTCCACTCAAGGCA | 8761 |
| Q _y | 9137 | AGCAGGAAAAUAAAAAUAAGAAAGUCGAGAGAAACAUGAGAAACAUTUCGAUA | 9196 |
| D _b | 8762 | TTGCGCCAAACAAATGGAGGCTTTTGAAACCGGCCGATGATCCCAACGGGCAAAAGCAAGCAAC | 8821 |
| Q _y | 9197 | CGGCAUCUGUGCUUUUUUCAAACAACGAAAAAGACAGGAUGUGCAUGUAGGAUCA | 9256 |
| D _b | 8822 | AAACT-----GTCAATCAATCTAGAAAAAAGATGTCAATGTTTGGCACAG | 8863 |
| Q _y | 9257 | GUGGAUCUUUUAUACCAAGAAUUAUUAUCGAUAUCCAUAUAAACUACAUAUCCCAANAG | 9316 |
| D _b | 8864 | TTGGTACTTTTGCAGTGCACGGTTAAAGGACTTTGNCACNAANAATGAGCATGCTTAGAG | 8923 |
| Q _y | 9317 | UGAAAGGAAAAAGAAUUUUAAAAUUUGAGUUCUUUUUAUAUAUACAACCAUGCAUAGUGG | 9376 |
| D _b | 8924 | TCAGAGGGAAGCAGCTATGAACTTAGATCACTTGTGTTGGTCTACACCCACGACGAAGTTG | 8983 |
| Q _y | 9377 | ACAUUACAUAUACGAGGCAAGUAUUUUAUCAGUUUAUAUACUGGUACAACCGCUUGAAGG | 9436 |
| D _b | 8984 | ACTTGGCTAAACAAGAGGGCTACAAAGGAAACAAATTTGACACATGGTATGATGGAGTTAAAC | 9043 |

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| Db | 1106 | CCATACGCAGAAAGANTACACACTACTCTGATCGAGGTGTCAAATTTTGGAAAGGTTTCG | 1161 |
| Qy | 1610 | AUCGUCAAUUUAUGACAUCUCGAGUAAGACCUAAGAAACGUCUACUGAGUGCAAGGCCACUA | 1669 |
| Db | 1166 | ACACAGCCCTTTCAACGATATAGAAA--ACAGGATCGTGAGCACACTTGTGAAACGGATC | 1222 |
| Qy | 1670 | UAAAGUUGGAGGUGUGCGGCAAAUGGCAGCCAUUGUAAACCAACUCCUAUUUCCAAUGU | 1729 |
| Db | 1223 | TTGACGTTGGAAGAGTGTGTCAGGTGTCTGCTTTATTGTGTCTCGCTCTGTCTTCATGTG | 1282 |
| Qy | 1730 | GGAAAAUAAACAUCACUACUUGUGGAGAAACUGCUUGAAAAUUGUUCACAAAGAGGAGAAAC | 1789 |
| Db | 1283 | GAAAAATPAACATGCATTAATGTGTAGAGGAAAACTGCTATCGAAGGTCAAGCGACAC | 1342 |
| Qy | 1790 | UGAAAUUUUCAGCGCGUAAAAAGGAGCCAAUUGGCAAGUAAAUUAUCCAGUCUCCUAUCA | 1849 |
| Db | 1343 | ATGAGAAATATACTCAGGAAAAACAACAGAGATAAGGCAAAATTGTTTTCCAGCGACATCCAC | 1402 |
| Qy | 1850 | AAUUUCCUACGUGAUCAUUUUCUUAUCGAUAUGAGAAUAGUCUAUCCAGUAGGAACA | 1909 |
| Db | 1403 | AGTTTAAACACGCTCTCGAGATACTAGAGAGCGCAAGTAAGGCCACTACAAGCGTGAATA | 1462 |
| Qy | 1910 | CAAAACUUCGAGCGCACAAAAACAAUUGCACAAAUUAUUGGCAGUCGCACAAAGAGAUUCCU | 1969 |
| Db | 1463 | GCAATTATAAGATTTTACAGAGATCACAGCCTCTCAGAAGGAAAAACACTCTCTGCTT | 1522 |
| Qy | 1970 | UUUCAAUUUAGAGCAUCUGAAUUGCUAAUUUAAUGCGGAUAAACUUGUAGCGAGG | 2029 |
| Db | 1523 | TTAGCCATGCAAGTCGTATAAATGATGTGCTAATAAAGGAGGCGAGTGCATGCTGAGG | 1582 |
| Qy | 2030 | AUUUCUAUAAAGUCUCAUUGCCUUUUAAGAGCUAACCGCUGGCAUAAAAACAGGAGCG | 2089 |
| Db | 1583 | AACATTCAGAAAGCAACACGAACCTTGCTGAAATTTGTCCGCTACTTTAAGAAATCGAATGG | 1642 |
| Qy | 2090 | AUUCAUUCAAGAAGGAGAGAUCCACAUUUCGGAUAUAAGUUCAGGUAAGGCAACAU | 2149 |
| Db | 1643 | AGAGTTCGGAAGAGGACATTGAAGACATTTCCGAATAAAATCTCTCAGAAGGECTCAAT | 1702 |
| Qy | 2150 | UUAAUUUUUGCAUUGUGUGACAAACCAACUUGACAAAAUUGGUAAACUUGUGUGGGUG | 2209 |
| Db | 1703 | TGAACCCAGCATTAAATGTGTGACAACTCAACTCGACGAGATGGGAATTTCTGTGGGGTG | 1762 |
| Qy | 2210 | AAAGAGGUUAUCAUGCGAAGAGGUUUUUUUUAAACUUUUUGAAGAAAGUUGAUUCAAACUG | 2269 |
| Db | 1763 | AAAGAGGATATCATGCTAAGCGGTTCTTCAACAAATACTTCGAAATTTGTCGATCCTAGCA | 1822 |
| Qy | 2270 | ACGCUUAUAGAACAACAUAUUGCGAGUCUACCCAAUUGGCACACAGACAAACAGCUUAG | 2329 |
| Db | 1823 | AAGGATATGAATAAATTTGAAACGCGCATCAACCCACAGAGCCACGCAAAACAGCAATAA | 1882 |
| Qy | 2330 | GAAAACUGAUUUUAUCGACGCAUCCUACGCUACGACAAACAAUUGAAAGGUAGCCCAA | 2389 |
| Db | 1883 | CTAGACTGTTGTCCCAACAAACTTTGAAGTACTTAAGGGAACAAATGCGGGGAGAAATCAA | 1942 |
| Qy | 2390 | UCAAGAGUUUCAGUUGGUUAAUUAUUGUACAAGCAAAAGAGAUUGGUUUAUCGCUUAC | 2449 |
| Db | 1943 | TTGAGAAACACCCCTTGACTGTTGAATGCAACAGTGTATTAATGGCGGATTTCTTATTCT | 2002 |
| Qy | 2450 | CAGCAUCGUGUUACAAGGAAGAGUAGCGCAUUGUUUUCUGAUUACAAGUAGCCAA | 2509 |
| Db | 2003 | CCTGTTGTGTGTTTCAAAATGAGTCTGGGAACCCCATATTTGTGAGAGTTACAGATGCCGA | 2062 |
| Qy | 2510 | CUAAGAAUACUAGUACAUUGGAAAUUCAGGAGAUCCAAAGUAUGUGUAGUACCAAGCA | 2569 |
| Db | 2063 | GGAAGAAATCATCTAGTTGTTCGGAACAGTGGCGAATCCAAATATGTTGATATGCCACCAC | 2122 |
| Qy | 2570 | GCUCAAGUGA---CAUGAUUUGUCUAAAGGAAGGUUAUUGUUAUCUCAAACUUUUCUUGG | 2626 |
| Db | 2123 | AGGATGACAATCTATGTATATAGCCAAAGCTGGATATTGTTATACAGAACATTTTCTCTGG | 2182 |
| Qy | 2627 | CAUUGUUCUGAUAUGUAGUAUGAGUGAUAUCAAAAUCAUUAUCAAAAGAGGUUAGAUUA | 2686 |
| Db | 2183 | CGATGCTTGTAAATGTCCGAAGGAAGAGCGCAAGCGTTTACAAAGATGGTCAGAGATG | 2242 |

| | | | |
|----|------|--|------|
| Qy | 2687 | UAAUUGUACCGGCUUCGUCGUAACUGCCNAGCUUAAUCGAUGUUGCCAAUGAAUGUUAUCU | 2746 |
| Db | 2243 | TGCTCATAAATCAGTTAGGGACATGGCCATCACTCTTGGATGTGGCAGCGCATGCTATC | 2302 |
| Qy | 2747 | UCCUAUCAGCCUUCUCCACCCUGAAACGAAAAUGCUGAGUUGCCCGGAAUUCUAGUGGAUC | 2806 |
| Db | 2303 | TGCTGAAGGTGTTCTTCCAGATGTTAGTGTGGCGGAGCTACCAAGAAATATGTTGACC | 2362 |
| Qy | 2807 | AUACAUCAAAAUUGAUUGAUGUAGUUGCAUUAUAGUGGCGUAGACACGCAAAUUAUCG | 2866 |
| Db | 2363 | ACAAAACAAGACAAATGATGTGATTCGTATGGTTTCATTTGAACACTGGTTATCATCA | 2422 |
| Qy | 2867 | UUUCUAGGCGAAAUAUCUAGUAGCAGCUAAUUAUUAUUGCCCGGAUAUGACUUGGAUUCGG | 2926 |
| Db | 2423 | TTTTAAAGCAAAATACGGTTGAGCAATGATCAAAATTCACAGTCGGGTTTAAATATCAG | 2482 |
| Qy | 2927 | AGCUGAAAAUUAUUUAGUAGUGGAGACCUCCAUAAGCAAGCAAGCUCUCA | 2978 |
| Db | 2483 | ATATGAAGCAATTACTTGATTGGTGTCCAGTCTAAACAAATGAGGATATTGACCCCAATAG | 2542 |
| Qy | 2979 | -----GUGUCCAUAAAUUACUCUGUAAUUGAUAUUAUAGGCUAAU | 3022 |
| Db | 2543 | AATATCGGACACCATCGTGGCAATTTAAAGAACTCATAAAGGCATATACACCCCAAG | 2602 |
| Qy | 3023 | UGAUGAGGCAAUUGAUGAGGAAGCCUUUUUUUUUUGAUUUUAGCGUUAUCUCCACGAG | 3082 |
| Db | 2603 | TTTTGCTCGATGCATTCGAAATTCAGACATATTTGCTCTTTATGCAGCTTTTACCAG | 2662 |
| Qy | 3083 | GUGUUUUUAUGUUUAUUAUAGUCAGUAUUUAAGAAUUAAGCUUUUAAGUACUGGAUA | 3142 |
| Db | 2663 | GTGTGCTCATTTGCAATGTGTAACACATGTCATCATTTGGAGATCTCTACTAGGGAGTACATGC | 2722 |
| Qy | 3143 | GCAAGCAACAGUCUGUCGUCGUUUUUUUGCAAUGAUCUUGAUCUAGGCAUAGCUCAAAAGUAA | 3202 |
| Db | 2723 | GGAAGGATGATGAATTCGTGGCAATTTGCTCATATTAGNATCACTTGGCGGAAAGTAT | 2782 |
| Qy | 3203 | CAGUUGCUCAACAUAUGAAUAGAGCAGAGACUAAUUAUCUUGAAACGCGGGGCGCCAAUUAUGA | 3262 |
| Db | 2783 | CGGTCTCCACTAGTTTGTGTCTCCAACTCACTTTGATTGAAGGAGAAGCTCAATATATCA | 2842 |
| Qy | 3263 | UUUCGGUACUGGAAACCAUACAUAGACAAGCC---AUUCAUACCAACCGCGCUUCUUC | 3319 |
| Db | 2843 | TTGAGCGAGTACAAGGATAAAACAGCGGTACCGATACCATACACAGTAGTGTATGGAGA | 2902 |
| Qy | 3320 | AACUACAGGCUAGGCAAAUCGUAGAGACAUAGAAUUCUUCUUGAUUCGCGCGGAUUA | 3379 |
| Db | 2903 | TGTTGATCATCTTGTGATCTAGATCTGAAATCAGATGCAGCACTTGTATGCAGCTGGCTTCA | 2962 |
| Qy | 3380 | GCAUUAUACAUCUGAUGAUGAUGUAUUGAUGGAAAAAAGUUAUUCUACUGGAUUAUG | 3439 |
| Db | 2963 | AGAAAGTTTCA---CGCGAAAGTGTACAACCTCATGGAATAAAATTTATCTAAGAAATCTTGG | 3019 |
| Qy | 3440 | AGGAUUCGUGGAAACGAUUUAAAGUUGUUGAAAAAUUAACAAGAAAUUGUGGCGCAUUAUCAA | 3499 |
| Db | 3020 | AGGACGAGTGGCGAGGATTGATTTGGCGGCAAAAATTTCTGCAATATTACGATCATCAAA | 3079 |
| Qy | 3500 | AGUACUAAUAUCUGGGAAUAGUCAAUUUCAAUGAAAGGCGCUACCGGAUUAUGGCGUUC | 3559 |
| Db | 3080 | AGTTTGGGATACATACACGCTGGTGGTTTGCAACACAAAAGCATCGAAGATTTAGGAGGCA | 3139 |
| Qy | 3560 | GAUAUUCAGUAUCGCAAGCAGUUUUAUAUCAUGAUGAAGAAACCGUUGCAAGAAUUCU | 3619 |
| Db | 3140 | GATACGGCGGAATCAATGAGTCTTATTTTGGAGAACTTTAAAAATGGAGCGCGCAATATGCAT | 3199 |
| Qy | 3620 | GUGUUAAGCAAGAGAUCAUUGUAAGGAAGUAAUCAUCAAUACAAUCCUGGCAUUAUC | 3679 |
| Db | 3200 | GCAAGAAACTCACCACACAACCCCAAGACAATAACCAAGCAGCACACAATATAAAGA | 3259 |
| Qy | 3680 | GGGCAACAUUUUUUUGUAGGUGGUGCUUGCCUGAUGUUGAAGUUAUUAACAUCG | 3739 |
| Db | 3260 | GAAGGTTGTACTCTCTGTTTCAACTACTTTCATTTCCAGATGTGTTCAGTTTATAAACGTGA | 3319 |

Db 3438 AGTTGGAGCTTGCAGAGCGGAGCGTTAAGAGATAGATAAATGGGAACCTCGCGTTCCACCAATT 3497
Qy 3872 AGGAGCAGUAAAGAU---CAAUCCAGACCCUGACAAAGAGGAAGAUUUUAGAGGAGUACAUUG 3928
Db 3498 CTATTCTAACTCAGAGTGCATAATCAGCATCCAAGTTTGACGAATTCGTTGCTACATCA 3557
Qy 3929 CAAGAAGUAGACCGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 3988
Db 3558 ACGAAAAGCACCCTCTCAGTGTAGTACATGATGTTTGAAGAGAGGCGAGTAAC---AC 3614
Qy 3989 AUCAAAGCUAAGCGCAGAGGAGGACAAACUUGGAGAGAAAUUAVAGCAUUGUUGCCUUG 4048
Db 3615 ATCAGGAAAGAGCGCTCCGAACAGAGCTCGAACGAATATAGCAATTCATCGCATAG 3674
Qy 4049 UUAUGAUGAUUUUUGACUCAGAGAGAAAGAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 4108
Db 3675 TGCATTATGATGTTTGAAGCGAGAACGAAAGCGACTGTGTACGAAAGATCCTCAACAACTAA 3734
Qy 4109 GAAUUCUGUUGCCACAUGAUGAUGAACUGUUGGCAUAUCAAAGCUUGGAGCAUAUUCAG 4168
Db 3735 AAGGATTTGGTGTCCACCGTGAACCTACTCTGTTTATCATCAGGCGCTCAACGACATAGAG 3794
Qy 4169 ACAUUCUGACUCAGAAAGAAACCAUUGAUUUGCAUUGAUGUAGUAGUAGGAGGAGCAAG 4228
Db 3795 ATGATCTTACGAGAGAAATCTCTTCGTGCTGACTTTGAACTCAGCAGTGATAGCGAGATGA 3854
Qy 4229 UUAACAGAUUCAAAG---GAGAUGAAAUUUGCCGCAUGGUGGAGAAACAAACUACAAUUG 4285
Db 3855 TTCAACAACCTGCCGCTGACGGACATTTGCATCATGTCGAGTCCACCACTAAGTAGGG 3914
Qy 4286 AUAGAGUUGUACCCAUUUUAGAACCAUUGGAGGAAAUUUUAGUAGUAGUAGUAGUAGUAGUAG 4345
Db 3915 GATTCACAATCCCACTACAGAAACAGAGAGAAATTCATGACCTTCCTACTAGAGCAACTG 3974
Qy 4346 GUGUAGUGUAGUAAACAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 4405
Db 3975 CCACAGAAAGTCGGGGTAAATAGCACATGAGAGCGACAGGACATACTACTATGCGGAG 4034
Qy 4406 GUGUAGUAGUAGGAAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 4465
Db 4035 CAGTGGGATCAGGTAAAGTCACTGCTGCGGTACCACTTTCCAGAAAGGAAACGTTG 4094
Qy 4466 UUAUGUCUAGCAACAAAGACCAUUGGACGAGAAUGUUCUACGACGAGUAGAGACAUC 4525
Db 4095 TACTTCTGGAGCAACTCGTCCGCTTGCAGAGAGATGTTCAAGCAATTTATCGCAAGCTC 4154
Qy 4526 CCUUUAUGCAACCCACAUUGAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGU 4585
Db 4155 CATTTTACCAGATATACAACTTTTAAAGATGCGAGGTTTGACAGCATTTGTTGTCAGCCAA 4214
Qy 4586 UAUUGUUAUUGACUAGUGGAAUUGCUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 4645
Db 4215 TATCAGTGATGACCAAGTGGCTTGCATTAATTAATTTGCAATATACAGAGCAGGATG 4274
Qy 4646 GUGAUUUUAGAAUUGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGU 4705
Db 4275 AAGAAATTTGACTTTGTTATATTTGACGAGTGCCATGTTTCAGATGCGCAATGCCATGGCAA 4334
Qy 4706 UCGUGUUCUUCUCAAAGACAAACUUAUGAUGGCAACUUAUGAUGGCAACUUAUGAUGGCAAC 4765
Db 4335 TGAGATGCTACTACAGAGTGCGATTAATTCAGGCAAAATCATCAAGTGTCCGCCACGC 4394
Qy 4766 CACAGGCGCGUGAAGUAGAAUUCACACAGACAGUCCAGUUCUUAUUAUUAUUAUUAUUA 4825
Db 4395 CACCGGTCCAGAAAGTTGAATTTCCACCACCAATATCTGTGACAAATAAGTACAGAGACA 4454
Qy 4826 AACUUAUUGUUCUUAUUGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGU 4885
Db 4455 CATTTGCTATTCAAGACTTTGTTAAACGCAACAGGTAGTGAAGTAAATGCGATGTGATTT 4514
Qy 4886 AUAAGGAGACAACAUUUUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGU 4945
Db 4515 CGAAAGGAGACAATATCTTTGTGTACGTGCTAGTTATATGAAGTGGACACACTATCGA 4574

Qy 4946 AAAUGCUCGAGAAAGGCUAUUUUAGUGACUAAAGUCGUAUGGCGUACCAUGAAAAUUG 5005
Db 4575 AACTTCTGGCTGAAGAGGACTTTAAAGTCCAAAAAGTCGACGGAAGAAACAATGAAGTTG 4634
Qy 5006 GUUCGACCCACCAUAGUUAUUAAGGAGGAGUAGCCAGAGAAACAAUUAUUAUUGUAGCAACCA 5065
Db 4635 GGAATATCGAAATATACAAAGTGGAAACCTAGCAAGAAAGCACTTCATAGTAGCCACCA 4694
Qy 5066 ACAUAAUUCAGAAUUGAGUACUCUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 5125
Db 4695 ACATAATTTGAATATGAGTCCACTAGACATCGAGTGTGTTGCTGACTTTGGACGAAAG 4754
Qy 5126 UCACUCUGGAAAUUUGAUUAUCGACCAACCGGUGGUAUUAUUAUUAUUAUUAUUAUUAUUA 5185
Db 4755 TACTCCGCTACCTCGACACGCAATAGAAATGCTTAGTAGTCAACAAAAACAAGCATTAAT 4814
Qy 5186 ACGGAGAACGCAUACAAAGAUUGGCGAGGUGUAGACACAGAAAGGCGCAUGCAUGA 5245
Db 4815 ATGGGAGCGAATCCAGAGACTAGGTAGAGTGGTAGGACAAACCAGGTCATGCTTTGC 4874
Qy 5246 GAAUUGGAAACUACAAUUAAGAUUAGAUUAGAUUAGAUUAGAUUAGAUUAGAUUAGAUUAG 5305
Db 4875 GAATCGGCCACACAGAAAGGTTTGAAGTCCCAAGTTCGATGCAACAGAGCGCG 4934
Qy 5306 CAUUUCAAUGCUUACAUUAGGAUUGCCUGUAAUUAUGACACAAGAGAUUUCAGUUUAACAGU 5365
Db 4935 CTCTTAAATGCTTCATATGACTTCCAGTGATTAACCAATATGTTTCAACAAGTATTC 4994
Qy 5366 UAUCAAAUUGCACAGUCCGACAGGCGAGUUAUUGUUCUUGUAGUAGUAGUAGUAGUAGUAG 5425
Db 4995 TTGGTAACTCAGTGAAGCAAGCAACGAACTATGTGAGTGTTCGAGATCAAGCCATTC 5054
Qy 5426 UUAUGSCUUAUCUUGUUAUUAUGAUGGCGAGCAUGACCCUGAGAAUUAUUAUUAUUA 5485
Db 5055 ACACAAGCCAGGTAGTGAGATAGATGGAATCAATGCACCACCAAGTGCAGCACTCTTGA 5114
Qy 5486 UUCUUUAACAAGUUAAGAAUUCUGAAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 5545
Db 5115 AGAGATTTCAAGCTCAGGGACTCTGAAATTTGCACTAAACAATAATAGCCATACCAATCGAG 5174
Qy 5546 UAAACAUCAUUUGGCUAGAUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 5605
Db 5175 GAGTGAATGCTTGGCTCAGAGCCAGTGAATACGCTGACTTGGCGCAATGTTGAGGACA 5234
Qy 5606 CGCGCAAGCAAAAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 5665
Db 5235 GCGGTGATGTGAGATCCCTTTTCATGTGCTGACATTCAGAAAAAATCCCATCTAGAAA 5294
Qy 5666 UUGGGAAGAUUUCUCAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 5725
Db 5295 TGTGGAGCTGTTGTGAAATTCAAAGGCGACGCGAGTTTGGGCGCTCTTTCAAGCGCAA 5354
Qy 5726 GCGCAACAAAAGUAGCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 5785
Db 5355 GTGCGAGTAAAGTAGCTCAACATTTGCAAAACAGATGTCAACTCTATCCAAACGAGTCA 5414
Qy 5786 GAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 5845
Db 5415 CCATCATTTGATATTAATTCGCTGAAGAGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAG 5474
Qy 5846 CAAGUAAACGAUAGUGGGAACACUUUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 5905
Db 5475 CATCTAATTTGCGTTCTTCTTCAAACTTTTCACTACAGAGCATCACAAAATGCAATAGAT 5534
Qy 5906 ACCAUUUGCUAAGGACUACACUGGCGCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 5965
Db 5535 CTCGTATGATGAAGATCAACATGTGAAAAATATATCAGTACTTGAAGGAGGCAAGTCGC 5594
Qy 5966 AAUAUCUGAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 6020
Db 5595 AATTACTTGAGTTTCAGGAACCTTGAATGCGAGACCACTCGTTCCACCACCAATCTGACGGAA 5654

Db 1398 CCATGAAGCAGCGTTGACACAGTTACGTGATGTCATTAAAGTCTAGTTATCCAGGTTTA 1457
Qy 1856 CUUACGUGGUAUCUUUUUUAUUGCAUUGAGAAUAGUCUGAAUUGCGAUGAAACACAAACU 1915
Db 1458 AACATGCAAGTCAAACTACTAGATAGATATGAACTACTGAGTGCAGTGAATAAAGT 1517
Qy 1916 UCGAUGGCGCAACAACAAUUGCAAAUUAUUGCGAGUCUCCAAAGAGAGAUUCCUUUUCAA 1975
Db 1518 ACCAGGATTTTCGAGAAATCCAGAGCATAAGCGATGGAGTGGAAAGCTGCAATCCAC 1577
Qy 1976 AUUUAGAGCAUCUGAUGAAUUGCUAAUUAAGUCGGAUAAUUCUUUAGCGAGAUUUCU 2035
Db 1578 AGTCAATAGCTGAACGCAATATTGATCAAGAGCTACAGCGACAGGGGAGGTTCT 1637
Qy 2036 AUGAAUUGUCUUAUGCCUUUAGAGCUAAACGCGUGCAUAAACAGGAGGAGUUCU 2095
Db 1638 CACAAGCCACGAAGCATCTACTCGAGATAGCAGTACCTGAAACACAGAACTGAGAACA 1697
Qy 2096 UCAAGAAAGGAGAGAUUCACUUCUUUCCGAAUUAAGUUGCAGGUAAGCAAAUUAUU 2155
Db 1698 TCAGAGAGGTTCCGTTAAGTCTTCGCAACCAAGGTTTCCAGAAAGCGCACATTAAAC 1757
Qy 2156 UUCAUUAGUUGUGACAAACCAUUGACAAUUAAGUUAUUCUGUGGGGUGAAAGAG 2215
Db 1758 CAACACTAATGTGTGACAAACAGCTCGACAAGAACGGAATTTCAATGGGGTGAGAG 1817
Qy 2216 GUUAUACUGCGAAGAGUUUUUCUAAUUCUUUUGAGAAAGUUAUUCUAAUCUGACGUU 2275
Db 1818 GTTATCAGCAAGCGCTTCTTTCAGCAATTTACTTCGAGGTAATTGATCCGAGNAGGTT 1877
Qy 2276 AUAAGAAACAUAUUGCGAGUACCCAAUUGGCAACAGCAAAACAGCUUAUAGGAAAC 2335
Db 1878 ACACCTAGTACGAAACAAAGAAATAGTACCAATGGATCGCGAAAGCTTGCAATTTGGTAAAC 1937
Qy 2336 UGAUUUUAUCGAGCAUUCUACGUAACGACAAACAAUUAAGUAGGAGCCCAUACAA 2395
Db 1938 TCATAGTCCCTACGATTTTGAAGTCTTAAGGGAACAGATGAGAGGTGAAACCGCGGAAC 1997
Qy 2396 GAGUUCAGUUGGUAUAUUGUACAAAGAAAGAGUUGUUAUUCUUAUUCAGCAU 2455
Db 1998 CGTATCCAAATTACAGTTGAGTGGTGAGCAAGTCAACAGGTGATTTGTCCATGCTGTT 2057
Qy 2456 GCUGUGUUAUUAUGGAAAGUUGUACGCAUUGUUUUUGUAUUAUUAUUAUUAUUA 2515
Db 2058 GCTGTGTGACAAACAGAGTCAAGTGTATCCAGTCTCTCTGAAATTTAAATGCCGACCAAC 2117
Qy 2516 AUCAUUAGUUAUUGGAAUUAUUGAGCAUCCAAAGUUGGAGUUAUCCAGCAGCUAA 2575
Db 2118 ATCATCTGGTGTGTTGATTAAGTGTGATCCAAAGTACATTTGATCTCCCTGAGATCGAGG 2177
Qy 2576 GUGACAUUAU--UGUGGCUAAGGAGUUAUUGUUAUUCUUAUUCUUGGCAUUG 2632
Db 2178 AGAACAGATGTATAGCGAGAGAGGTTATTGCTACATCAATCTCTTACGTATGT 2237
Qy 2633 UGUGAUGGAAUUGAGUGAAUUCAAUUAUUCACAAAGAGGUGAGAUUAUUAUUG 2692
Db 2238 TGGTTAATGTTAAGGAGCCGACGAAAGGAAATTCACGAAAGTTGTCGAGACAACTAG 2297
Qy 2693 UACCGGCUUGCUAUGGCAAGCUUAUUGAGUUGCAUUGAAUUGUUAUUCUUAU 2752
Db 2298 TTAGCGAACTTTGGTAAATGGCCCTCTCTGTAGACGTCGGCGACTGCTGTTATTGTA 2357
Qy 2753 CAGCUUCCACCCUGAAACGAAUUAUUGUUGUUGCCGAAUUAUUGAGUUAUUAU 2812
Db 2358 AAGTGTCTATCCNAGCGTCTTACGCTGAGCTACCAACGCTGTTAGTGGACCAAGA 2417
Qy 2813 CAAAAUUAUGUAGUUAUUAUUGGCGUAGACACGCAAAUUAUUAUUGUUAUUG 2872
Db 2418 CAAAGATAATCCAGCTGTTGATTCGATGGTCACTCTCGACTGGATATCATGTTCTTA 2477
Qy 2873 AGGCAAAUUAUGUUAUUAUUAUUGCCGAAUUAUUGAGUUAUUGAGUUAUUGGAGCUGA 2932
Db 2478 AGACAAACACTGTGGAAACAACTCATCAAGTTTACAAAGTGCATTCGAGTTCGAGCTTGA 2537

Qy 2933 AACAUUAUUAUAGUAGUGGA-----GACCUCCAUAGCAAGCAAG 2971
Db 2538 AACACTACCGCGTCGGGGAAACGGAATGGGAGAACGCTCACGGAGCTGATAACATAGATA 2597
Qy 2972 CUUCCAGUUGUCCAUAAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3031
Db 2598 ATCCAAGTGGTGTCTTAAGAGACTCGTGAAGGAGTGTACAGCCAAAGCAGTTAAAGG 2657
Qy 3032 AAUGCAUUGAGGAAAGCCUU 3091
Db 2658 AAGACATGTTGGCAAAACCCCTTTTACCACTGTACCACTTATTTGTCCACGAGTGTATCC 2717
Qy 3092 UAGCUUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 3151
Db 2718 TGGCTTTTCAATAGTGGTTCACATAGATCTTAATGAACCACTTATATTGGAGCAGATA 2777
Qy 3152 AGUCUGCCUCUU 3211
Db 2778 GTAATGTAGCCGTGCTGTAGTTGCTTGAAGTCTCTGGCACAGAAGTGTCAACAGTC 2837
Qy 3212 AAACAUUUAUAGAGCAGACUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3271
Db 2838 AAAGCGTTTGGCTCAGCTTCAATCATTTGAAGTGTCTGCTGAACTCGTTGAAGCTA 2897
Qy 3272 UGGAACCAUACAUAGCAAGCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3331
Db 2898 GAGCCAAACATCAATGGACCAAGTGGCGAGCTCTCGGGCGTGTAAACAGATTCTATGGCA 2957
Qy 3332 UGGCAAAUUGUAGAGCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3391
Db 2958 TGGCTTCTGCACATGGCGAGAACCAACTATGAAGTTCGCAACCGCGGATATACAACTCTGA 3017
Qy 3392 CUGAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 3451
Db 3018 GAGATCAGATATCTCCATCTTGAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3077
Qy 3452 ACAGCUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 3511
Db 3078 ACAGTAAAGTGGTGGCGAGCTGTGTTAAGATACTACTCTCAAGCAAGCAATCT 3137
Qy 3512 CUUGGUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 3571
Db 3138 TTACACAGAAAGATTTGCCAATGCAAAAGCGGAGCCGATTTAGCGCGACATACAGCGCT 3197
Qy 3572 CUGCAAGCAGUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3631
Db 3198 CGTCAATCTCTTACGAAATGGAGCAACACGCAAGCAAAAGAGTGAATCTGTATAG 3257
Qy 3632 GAGAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 3691
Db 3258 CTAATAAATCGCTAGTAGTATGTCGTGGACAGTAGCAAGTTTCAAAATAGTGTGTA 3317
Qy 3692 CUUUGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3751
Db 3318 GGAATAATAATTTAGTGCAGAGCGTGTAGATTATTAAGACGTTAGTTTGTGATTA 3377
Qy 3752 GUUUGAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3811
Db 3378 GCTTGTAAATCAAAATGACTGCTGAAGCTAAACCAATTTGTCAACGCAAGAGGCTGA 3437
Qy 3812 AGAGAAAGCAGAGGUGA--AUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 3869
Db 3438 AGCTGACATTTGAAGAAACGAGCGACGAAAGATCGAGTGGGAACCTCGCACTTTCCACT 3497
Qy 3870 UAAAGGAGCAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3928
Db 3498 CCATGCTTACGCAAAAGTGCAGGCAACACCCAAACCTGATGATTTACAGCTTATATTG 3557
Qy 3929 CAAGAAGUAGACCUUGAGCUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 3988
Db 3558 CTGAGAAAGCAGCCGCACTTAAGTGAAGATATCGAACCCGA---GGAAAGAGCAGTAGTCC 3614

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| Qy | 1496 | UUAGGGUAGCAUGGAGGCGGAGAAUUAUUGACG |
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| Qy | 1856 | CUUACUGGACAUUUUUAUUAUCCGAUUAUGAG |
| Db | 1458 | AACACGACGTGCAGATACTAGTAGGTATGAGCG |
| Qy | 1916 | UCGAUGCGCACACACAAAUUGCCACAAUAUUG |
| Db | 1518 | ATCAGGATTTTCGAGAAATTCAAAGTCTGACTG |
| Qy | 1976 | AUUUAGAGCAUCUGAAUGAAUUGCUAAUUAAGU |

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|----|------|--------------------|---|------|
| Db | 1578 | ATCGAAACAAGATTCAA | CGCTATATAATAAAGGAGCTACAGCAACAAGGTGAAGAGTTTG | 1637 |
| Qy | 2036 | AUGAAUUGUCUAUUGC | UUUUAAGCUGAUAACGCGUGCAUAUAAAAACAGGAGCGAUCAU | 2095 |
| Db | 1638 | AACAAGCAACA | AAACATTTGCTGTAAGAAATACCCCGATACATGAAGAATCGCACGTGAGAATA | 1697 |
| Qy | 2096 | UCRAAGAGGGAGAGAU | CACCAUUCUCCGAUUAAGUUGCAGGUAAAGCAACAUAUUAUU | 2155 |
| Db | 1698 | TTGAGAGGGGTCA | TAAAGTCTTTAGAAAAAATAATCCAGNAGGCACACATTAACC | 1757 |
| Qy | 2156 | UUGCAUUGAUGUGUGA | CAACAACUUGACAAAAAUGGUAACUUCGUGUGGGUGAAGAG | 2215 |
| Db | 1758 | CAA | CATTGATGTGCGACAATCAGCTCGATAAGAACGGTAACTTCATATGGGTGAAAGGG | 1817 |
| Qy | 2216 | GUUAUCAUGCGAAGAGG | UUUUUUUAACUUCUUUGAGAAAGUUAUUAACUGACGGUU | 2275 |
| Db | 1818 | GTTATTCAGCAAAAAGAT | TTCTTCAGCAACTACTTTTGAACCTTATTTGATCCAAAGAGGGAT | 1877 |
| Qy | 2276 | AURAAGAAACAUAU | AGCGAGUACAACCAAAUGGCAACAAGCAACAACAGCUAAGGAAAC | 2335 |
| Db | 1878 | ACACTCAGTACGAA | ACAAGAGTAGTGCCAAACGGTTCAGAAAACTTGCTATTGGGAAGC | 1937 |
| Qy | 2336 | UGAUUUUAUCGAGGAU | CCAUCUACGCUACGACACAACAAUAGAAAGGAVAGCCCAAUACAA | 2395 |
| Db | 1938 | TCATAGTTCGACAAA | CTTTGAAGTTTGAGAGAGCAATAGAGGGGAACCTGTAGAAC | 1997 |
| Qy | 2396 | GAGUUCAGUUGUAUUAU | UGUAACAGCAAAAGAGAGUUGUUAUCGUUAUCCAGCAU | 2455 |
| Db | 1998 | CACACCCAATCACA | GTAAGTGTGTGAGCAAGTCACAAGGTGACTTCGTCCTCATGCTATTT | 2057 |
| Qy | 2456 | GCUGUGUACAUAUGGA | AGUAGCGCAUUGUUUCUGUAUUAACAAGUAGCCCAACUAAGA | 2515 |
| Db | 2058 | GTTGCGTTACACCA | ATCAGTGTCTTGTCCAGATATCAAAATGCCAACTTAAC | 2117 |
| Qy | 2516 | AUCAUCUAGUCAUUGG | AAAUUCAGGAUCCAAGUAUUGGUGUAUCCAAGCAGCUCAA | 2575 |
| Db | 2118 | ATCATCTGGTAA | TCGGAAACAGCGCGACCGGAAATATGTCGATCTCCAGAAATCGAAG | 2177 |
| Qy | 2576 | GUGACAUAAU--- | GUGGCUAAGAAAGUUAUUGUUAUCUACAUAUUUCUUGGCAUGU | 2632 |
| Db | 2178 | AGAA | AAAAATGTATACATAGCCAAAGGAGGTATTTGTTACATTAACATATTTCTCGCATGC | 2237 |
| Qy | 2633 | UGCUGAAGUGAUGAG | AGUGAAUCAAUAUACAAGAAAGGUUAAGAUAAUUG | 2692 |
| Db | 2238 | TAGTAAATGTCAGGA | ATCAAGGCAAGGATTTACAGGTTGTCCAGGCAAAATTAG | 2297 |
| Qy | 2693 | UACCGCUCUGGCUA | UUGGCCAAGCUUAAUCGAUGUUGCAACUGAAUGUUAUCUCCUUAU | 2752 |
| Db | 2298 | TCGCGGAAC | TAGGTAAGTGCGCAACGCTATTAGATGTTGCAACGGCTTGCTACTTTCTAA | 2357 |
| Qy | 2753 | CAGCCUCCACCCUG | AAACGAAAUUGCUGAGUUGCCCGAAUUCUUGAGUGUAUACAUA | 2812 |
| Db | 2358 | AAAGTGT | TTTTTACCAGATGTAGCCAATGCTGAATTGCCAAAGGATGTTGGTGCCACCAATAAA | 2417 |
| Qy | 2813 | CAAAUUAUACUAGU | AGUAUUAUAGCUCGCUAGACAGCAAUUUAUGUUCUGA | 2872 |
| Db | 2418 | CAAAAGATCATC | CGATGTTGATTCATAGATCGCTATCAACTGGGAATACCAATCTTGA | 2477 |
| Qy | 2873 | AGGCAAAUACUGUA | AGCUGAUAUUAUUCGCGGAUUAUGACUGUGAUUCGGAGCUGA | 2932 |
| Db | 2478 | AAACAACAACAG | TTGAGCAACTCATTAAAGTTTACAAGACAAAATCTTTGAGTCAAGCTTGA | 2537 |
| Qy | 2933 | AACAUUAUUNAG | UGGUGA-----GACCUCUAUAGCAAGCAAG | 2971 |
| Db | 2538 | AGCACTACCGTGT | TTGGGGGCAACAAGTGGGAAGACACTCATGGAGCCAAATAACATAGACA | 2597 |
| Qy | 2972 | CUCCUCAGUUGUCCA | UAAAUUACUCUGUAAUUAUUAUAGGCCUAAAUUAUGAGAGGC | 3031 |
| Db | 2598 | ATCCACAATG | TGCTAATAGAGACTCATAAAGAGGAGTGCACAGACCAGCAATTAAGG | 2657 |
| Qy | 3032 | AAUGCAUUGAGGA | AGAGCCUUUUUUGUUAUUUAGUGGUGUAUCUACACGAGGUGUUUAU | 3091 |

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|----------------|------|--|------|
| D _b | 2658 | AGGACATGTTGCCTAACCCCTTTTCTCACCATTATATGCTTTACTCTCACCAGGAGTTATTTT | 2717 |
| Q _y | 3092 | UAGCUUAUUAAUAGUCAGCAUUTUAGAUAUUGCUUAAAAGUACUGGAUCAGCAAGCAAC | 3151 |
| D _b | 2718 | TGGCATTTCTACAAGTGCGGTCTCTTAGAATACTTTGATGAACCACTACATCAAAGCAGACA | 2777 |
| Q _y | 3152 | AGUCUGUCGUCGUUUUUUUGCAAUUCAUGGCAUUGCUGGCAAAAGUAAACAGUUGCUC | 3211 |
| D _b | 2778 | GTAACACTGCTGTGTTGTTAGTTGTCTTTGAAATCTCTAGCAAAAGGAGGTCTCAGCAAGTC | 2837 |
| Q _y | 3212 | AAAAUUAUGAGCAGAGACUAUAUACUUGAAACGCGGGGGCGCAUUAUUGAUUUUCGUGCA | 3271 |
| D _b | 2838 | AAAGTGTTGTTGGCGCAGCTTCAAGTCACTCAGAGGAAGCCTGCCAGAACTTTGTTGAGGCAA | 2897 |
| Q _y | 3272 | UGGAAACCAUACACAUGACACAAGCAUUAUACAAACCCGCGCUUUAUUAACUACUACAGUGCA | 3331 |
| D _b | 2898 | GAGCCAACATCGTTGGCCCCAGACAGTGCAGCTTCTCAGGCATGTGCAACAAATTTCTTTGGTA | 2957 |
| Q _y | 3332 | UGGCAAAUCGVAGAGACAUGAAUUCUUCUUGAUUCUCGCGGAUUCAGCAUAUUAUAAU | 3391 |
| D _b | 2958 | TGCTTTATTCATGTCTCAGAACCAACAAACAACTTGCAGTGGCGGTACACGATTTTAC | 3017 |
| Q _y | 3392 | CUGAAGAUAGUAGUUAUUGGAGUGAAAAAGUAUUAUCUUAUGGAUAUAGAGGAUUCUGGA | 3451 |
| D _b | 3018 | GAGATCACAGTATCAGCTATTTCTGGAaaaaagctatctgcagatcttttggacgaagcatgga | 3077 |
| Q _y | 3452 | ACGACUUAAGUGUUGGAAAAAUAACAAGAAUGUGCGAUUAUCAAAGUACUACAUAU | 3511 |
| D _b | 3078 | GCGAGCTAAGCTGTGCGAGCGTTTGCTGTATAAATACTACTCATCAACGAAGCAATTT | 3137 |
| Q _y | 3512 | CUGGGAUAAGUCAACUUUUAAGAAAGCGCCUACCGAUUAGGCGGUGCAUUAUUCAGUAU | 3571 |
| D _b | 3138 | TCTCACAGAGAGATTTGCCAATCAAGCGCGCTCGATTTTAGCGCGCAGATACAGCGAGT | 3197 |
| Q _y | 3572 | CUGCAAAAGCAGUUAUAACAUCAGUGAGUAGAAAACUGUCAAGAAAUUUUGUUAAGCAAA | 3631 |
| D _b | 3198 | CAGTCATATCTCTCAGCAATGGAGTAGGCAACGATGAAGAGA--CTGTATTTCTGCTAT | 3255 |
| Q _y | 3632 | GAGAUACUUGUAAGGAUAUAUCAUAUACAACAUCCUGGACAUUUCGGGCAACAUAUU | 3691 |
| D _b | 3256 | GTGCAACAAACACGCAACAGCTGTGCTCTTGGATGAGTGTGTAATAATTTCCAGTAGTGTTG | 3315 |
| Q _y | 3692 | CUUU--GUGAGUGUGUGUCUGCUAGUUUUUUGAAGUUUAUAAACAUAGCUUAUAGUAU | 3749 |
| D _b | 3316 | TAGAACCATCAACTATTTAGTGCCAGATGTTTTCAAGTTTTATTAAATGTACTCGTAGTCAT | 3375 |
| Q _y | 3750 | AAGUUUAUUCNAGCAUUUGCANUUCAGCUAAUUAUUAUUGGUUGCAUUAUGCACAUAU | 3809 |
| D _b | 3376 | CAGCTTACTAATCACCATAGCCTCTGAAGCTAATCTGTATCGTCACAGCGCAAGAAGCT | 3435 |
| Q _y | 3810 | GAAGAGAAAAACGAGGUGAUAUCGAGAAGUUUCUGAUAUAUUAUUAAGUUGCCCUCA | 3869 |
| D _b | 3436 | CAAGTTAGAGCTTGGGAGACGGAGCGTAAGAGATAGTGGGAACCTCGCTTTTCACCA | 3495 |
| Q _y | 3870 | UAAGGAGCAUUAAGA--UCAUUUCAGACCCUGACAAAGAGAAAUUAUUAAGGAGUACA | 3926 |
| D _b | 3496 | TTCTATTCTAACTCATAGTGCAATCAGCATCCAAACGTTTGTATGAAATTCGTTGCAATAT | 3555 |
| Q _y | 3927 | UGCAAGAAGUAGACCGUAGUGUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA | 3986 |
| D _b | 3556 | CAAGCAAAAAGCAGCCCATCTCAGTGAGTACATTTAGTTTGAAGAGAAGGACAGTAA---C | 3612 |
| Q _y | 3987 | UCAUCNAGCUAAGCGCAAGGUAACAAAACUUGGAGAAAUUAUUAAGCAUUAUUGUUGCUU | 4046 |
| D _b | 3613 | ACACGCGCAAAAGGCAATCCGAACAAAGAGCTCGAACGAATCATAGCATTCATCGCATT | 3672 |
| Q _y | 4047 | AGUUAUGAUUUUUGACUCACAGAGAAAGAGUAGUUGUUAUUAUUAAGACACUGAACAAUU | 4106 |
| D _b | 3673 | AGTCTCATGATGTTTGTATGCAGNAACGAAGCAGCTGTGTCCAGAGATCTCTCAACAACT | 3732 |
| Q _y | 4107 | GCGAAAUUCUGUUGCCACAUGUAGUAGAACCUUGCGCAUCAUCAAAGCUUGGACGCAUUA | 4166 |
| D _b | 3733 | AAAAAGGATTGGTATCCACTGTGAGAACCTACTGTTTATCACCAGGCACTTAACGACATAGA | 3792 |

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| Qy | 4167 | AGACAUCUUGACUGACAAAGAAACAAACCAUUGAUUUUCGACUUAUUGAGUUGAGGGGAGCAA | 4226 |
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| Qy | 4227 | AGUUACAGAGUUCAAAG---GAGAUGAACUUUUGCGCAUGUGGGGAAACAAACUACUAAG | 4283 |
| Db | 3853 | GATTCAACAACTTCGCGCTGAACGAACATTTGTCATCATGTGGGAGTCACCACTTAAGTAG | 3912 |
| Qy | 4284 | UGAUAGAGUGGUACCCCAUUAUAGAACCAUGGGAAAUUAUUGAAUUCACUCUGUAGAAAG | 4343 |
| Db | 3913 | GGGATTTTACATCCCACTACAGAACAGAGGAAATTTATGACTTTCTACTAGACGAC | 3972 |
| Qy | 4344 | CUGUUGUAGUGUGAGUAAACCAUAUUCUUAUGCCCGCCUGAGAGAAUUGGAUAGUCGUGG | 4403 |
| Db | 3973 | TGCCACAGAAGTTGCGGCTAGATAGCACATGAGAGCGCACAGGACATATCTACTCATGGG | 4032 |
| Qy | 4404 | UGGUUGUUGAUCAGGAAAUUCUACUGUGUUAACUUCGUGUUAUCUUGAUAAGGCGCAGU | 4463 |
| Db | 4033 | AGCGTGGGATCAGGTAAGTCAACTGGTTTGGCGTACCACTTTTCAGAAAAAGGAAATGT | 4092 |
| Qy | 4464 | UCUUAUCUCUGAACCAACAAGACCAUUGGCGAGAGAAUGUCACGACAGUUGAGACAACA | 4523 |
| Db | 4093 | GTTACTTCTCGAACCAACTCGTCGCTTTCGAGAGATGTTTCATAGCAATTTATGCGAAGC | 4152 |
| Qy | 4524 | UCCUUUUUUGCAAAACCCCAUUGAGAGUUGCGAGGAAUGCAUUCUUUGGAUCUAGUAA | 4583 |
| Db | 4153 | CCCATTTTTCCAGAAATACAACCTTTAAGAATGCGAGGATGACAGCATTTGTTGTCGGCACC | 4212 |
| Qy | 4584 | UAUAUGUAUAUGACUAGUGAUUUUGUUCAUUAUUAUUUGCAAUAUAUCCUUAUUAUU | 4643 |
| Db | 4213 | AATATCAGTGATGACAGCAGTGGCTTTGCACTTTAACTATTTCGCAATAAACAAGAGACGCAAT | 4272 |
| Qy | 4644 | AAGUGAUUUGAAUUTUGUAUAUAGAGUAGUGUCACGUCUUAUGAGUAGCAACGUAUGGC | 4703 |
| Db | 4273 | TGAAGAAATTTGACTTTGTGTATTATTGATGAGTGCCATGTTTCACGACCCAAACGCCATGGC | 4332 |
| Qy | 4704 | AUUCGUGUGUCUUCUCAAAGAAACAAACUAUGAUUGAGCGAAACUAUUGAAAGUGUCAGCCAC | 4763 |
| Db | 4333 | AATGAGATGCTATTATCATGAGTGCATTTATTCAGGCAAAATCATCAAGTGTGACGCCAC | 4392 |
| Qy | 4764 | ACCAAGGCGCGUGAAUUGUAUUAUCCACACACAGCAUCCAGUUUCCAUUCAUUAUAGGAA | 4823 |
| Db | 4393 | GCCACGGGTCGAGAAATTGAAATTCCTCCACCCCAATATCTGTGCAATAATAATACAGAAGA | 4452 |
| Qy | 4824 | ACAAUUAUUUCCAAAGCUUUUUGAGACUCACAGGAAUGGGGUCUCACGAGUAGUAAU | 4883 |
| Db | 4453 | CACACTGTCTATTCACAGACTTTGAAACGCAACAGGTAGTGGAAAGCAACTTGCATGTGTAT | 4512 |
| Qy | 4884 | CAAUAGGGGAGACAAACUUUAGUGUUAUGUUUUAUUAUAGAGGUUAUUAUUCAGUCUCUC | 4943 |
| Db | 4513 | TTCCGAAAGGAGACATATCTTGTGTACTGTGGCTAGTTATATGAGTGAGACACACTCTC | 4572 |
| Qy | 4944 | AAAAUUCGCGAGUAUAAAGGCUUUUAGUGACUAAAGUCGUGGGCGUACCAUGAAAAU | 5003 |
| Db | 4573 | GAAACTTCTAGCTGAGAGGGACTTTTAAAGTCACAAAAAGTCGACGAGAGAAACAATGAAGT | 4632 |
| Qy | 5004 | UGGUUCCACCGACUAUAGUUAUUAAGGGAGUAGCCAGAGAAACAUUUUAUUGUAGCAAC | 5063 |
| Db | 4633 | TGGGAATATTGAAATTACAACAGTGGGACACCTTAGCAAGAAGCATTTTCATAGTAGCCAC | 4692 |
| Qy | 5064 | CAACAUAUUCGAGAAUGGAGUCACUUAUAGUAGUAGUUGUUGGACUUAUUGGUUUGAA | 5123 |
| Db | 4693 | CAACATTAATTGAAATGGAGTGACACTAGACATTTGACGTGGTGTGCTGACTTTTGGACGAA | 4752 |
| Qy | 5124 | AGUCAUCUGGAAAUUGAUUACGACAAACCGGUGCGUUUAUUAACAAGAACCCAGCAUUC | 5183 |
| Db | 4753 | AGTACTCCCATACCTCGACCGGATAATAGAAATGCTTTAGTAGTACAACAAAAACAAGCATTA | 4812 |
| Qy | 5184 | AUACGGAGAACGCAUAACAAGAUUGGCGAGGUUGUAGACACACAGAAAGGGCAUGCAU | 5243 |
| Db | 4813 | TTATGGGGGAGCGAATCCAGAGACTAGGTAGATTGGCAGGCACACAAACACAGGTATGCTTT | 4872 |

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| Qy | 5244 | GAGAAUUGGAAACUACAAUUAUAAAGGAUUGAUAUGAGAUUUCUAGUUCUUGUGCGGACACAGGC | 5303 |
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| Qy | 5304 | UGCAUUAUAGUUCUACAUUAUGGAUUGCCUGUAUUGACACACAGGAGUUAUCAGUUAACAG | 5363 |
| Db | 4933 | CGCTCTTAAATGCTTACATATGAGCTTCAGTGTGATCCCAATTAATGTTTTCGACAGATAT | 4992 |
| Qy | 5364 | UUUAUCAAUUUGCACAGUCCGACAGGCCAGAGUUUAUGUCUUGUUUGUGCGGCCUUA | 5423 |
| Db | 4993 | TCTTGGTAAGCTCACAGTGAAGCAAGCAGGACTATGTCTAGTCTTCGAGATCACGCCATT | 5052 |
| Qy | 5424 | CUUUAUGGCUUACAUUGUUAUAUCAUGAGCGACAGUACCCUGAAUAUUAUCAAGCAUUU | 5483 |
| Db | 5053 | TTACAACAAGCCAGGTAGTCAGAGTACGACGGTCAATGTCACCCACAAGTGCACGCACTCTT | 5112 |
| Qy | 5484 | AUUUCCUUAACAAGUAGUACUCGAAAUUACAUIUAGUCCCAUGGCUUUUAACUUUAC | 5543 |
| Db | 5113 | GAGAGATTCAAGCTCAGGGATTCTGAATTTGCACTAAACAAGTTAGCCCATCAACAACCG | 5172 |
| Qy | 5544 | CGUAAACAUCUAUUGGCUAGAUUGUAAAUUUUUAUGACAGUAUAGGAUCCAUCUUGAUUU | 5603 |
| Db | 5173 | AGGAGTGAATGCTTGGCTCACAGCCAGTGAATACGCTCGACTTGGTGCAAAATGTTGAGGA | 5232 |
| Qy | 5604 | ACCGCGGAAGCAAAAUAUCCAUUCCAUUGUAGAGAAUCCCAAGUAUGAAUAUACGACA | 5663 |
| Db | 5233 | CAGCGGTGATGTGAGAATCCCTTTCATGTGTCGTGACATTCACGAAAAAACTCCATCTAGA | 5292 |
| Qy | 5664 | CUUUGGGAAGAUUUCUACAAAUAUCAGAGCAUAAUUUUUUUGUUAUGAUGAGUGUUGU | 5723 |
| Db | 5293 | AATGTGGGAGCTTGTGTTTCAATTTCAAAGCGCAGCGAGCTTTTGGGCGTCTTTCAAGCGC | 5352 |
| Qy | 5724 | UAGCGCAACAAAAGUAGCAUUAACAUAAAACAGACAUUUAUUAUUGGAAAAACUCU | 5783 |
| Db | 5353 | AAGTCGAGTAAAGTAGCTTACATTTGCAATGCAACAGATGTCACTCTTATTCACGACAGT | 5412 |
| Qy | 5784 | CGGAUAUAUUGACGCCUUCUUGCAAGAAGAAUAUAGAAAAACAGCAUUAUUUUAAGCAU | 5843 |
| Db | 5413 | CACCATCATTTGACATTAATCGCTGAAGAGAGAAAGAAAGCAAGAAATCTTCAAGACAGT | 5472 |
| Qy | 5844 | GACAAUUAACGAUAGUGGGAACAUUUUUAUUGCUAUGCUAUGCAUAGCAUUAUACG | 5903 |
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| Qy | 5904 | GAACCAUAUGCUAAGGACUACACUGUGGCAUAUUAUCAGAAAUUGCAGGACGACAAAGAA | 5963 |
| Db | 5533 | ATCTCGCATGATGAAGATCACATCTCGGAAACATCTCAGTCTCTTGAAGGACGAAGTC | 5592 |
| Qy | 5964 | UCAAAUACUGGAUUCGCUAAUUUUAAUUCUGAUCCUUGCGGA-----6007 | |
| Db | 5593 | GCAACTGCTTGAATTCAGGAACCTTAAATGACAGACCATTCGTTCCACCACCAAGACCGATGG | 5652 |
| Qy | 6008 | -----AUUGCGGAUUCACAGAUUCGGAGUUCGUUAAGCAUUAUACCAUACGAGCAG | 6059 |
| Db | 5653 | GATTTCTCGAAGCTTTATGATGATGAGTACGGGACACTCGAAGCAGTAGTACCCATCAAAAGCAC | 5712 |
| Qy | 6060 | GCAAGAAAUUCAAUUUUAUUCUGAGAGUUAUGGAAUAAGUCAUUAUUAACAG | 6119 |
| Db | 5713 | CAATGATATGAGCAAGTCTTAAAGCTGAAGGCAAAATGGAAACAGAACCTAATCAAG | 5772 |
| Qy | 6120 | UGAUUUCUAGUUUUGUJAGGUGUCACUUAUGUGUGUUUCUGAGUAUAUGGGAUAGUU | 6179 |
| Db | 5773 | AGATGATTGGTTCATATGCGCGCTTCTTGAGGTGGAAATTTGGATGATCATACAGCGATT | 5832 |
| Qy | 6180 | CAAAUCAAACAUUGAAGAA-----GUUCAUUAAGAAAGAAAGGAGGAAAGACUCUAAAA | 6230 |
| Db | 5833 | GCAATCTGTTATTTACGGAGGCCCGCTTACTCATGAAGCAAAAGGCAAGAGACAGAGACAAA | 5892 |
| Qy | 6231 | GCUUAUAUUUUGGAGUUCGCGAUAAAGAAAAUUGGUGGAGAGUAUAUUGGAGACCG | 6290 |
| Db | 5893 | GTTGAAATTTTCGCAATGCTCGAGACCAAGATGGGTGAGAAAGTCTATGGAGATGACGA | 5952 |
| Qy | 6291 | UACUAUUGAAACAUUAUUUUGGACGCGCAUACGUCACAGAGAGGUGUGCAUUAAGGCCAGAA | 6350 |

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Query Match

Best Local Similarity 22.7%; Score 2304; DB 14; Length 9797;

Matches 3523; Conservative 1268; Mismatches 3770; Indels 105; Gaps 12;

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Db 992 AAGAGGGTCATAAACCAGGAATAGTGTGTGCTGGTGGAGTGAATCGTCATTAGGGAC 1051

QY 1447 GAUAGUUUAGAGGUUUGAGUGGACGCAUUUCGGAAGUUAUCAUUGUUGAGGUGAC 1506

Db 1052 GGAGCTTTAAATTCAGAGCAAGCAGGAGTCCATCAAAGCTTTTGTAAATCAGAGGTGAG 1111

QY 1507 AUGGAUGCAGAAUUAUUGCGUCUCUCAAAGAUCAACACACAGCGUUUAUGAACAAUG 1566

Db 1112 CATGAGGTAACTGTACGATGCCAGGATTAATAATTACAAGACGATGAGTCATAAGATC 1171

QY 1567 ACCCAUACAGUGAGCGAGUUUGAGUUUUUGAAGGUUUUGAUCGUAUUAUUGAC 1626

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Db 1349 GATTGTGTACTGATAGTGTAGCTATCCCAAGGACAAGCGAGCGAGCCATCCATGAAGAAT 1408

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Db 1409 AGACTGGCACAAATTCGCTGAGATTATCAAGTCGAGTTATCCACGCTTCAAGCACCAGTA 1468

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[illegible]

| | | | | |
|--------------|---|--|--------------------------------|-----------------|
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| Db | 9239 | GCCAAAGCCCATTTAGCGAGATAATGGCCCATTT | CAGTGCAGTGGCTGAAGCGGTACATTT | 9298 |
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| Db | 9299 | GAAAGCGTAACCAAGACCGACCATATGCCACGATAT | GCTCTTACGCGCAATTTTAAACC | 9358 |
| Qy | 9715 | GACAUGAUUUGCGCGCAUAUGCUUUUGAUUUUCU | UUGAUAUUAUGAACAAGGACGCCAGCU | 9774 |
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| Db | 9419 | CGTCCGAGAGGACACATCTCCAGATGAAGCAGCAG | CACTGCGTGGCGCAATATACAAT | 9478 |
| Qy | 9835 | AUGUUGGACUGGAUGGAAAAUGCGGAAUUGCGA | CUGAGAACACGGAGCGCCACACCGCA | 9894 |
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| Qy | 9955 | UAAGCAUAGUUUAUCUAGUAUCUUU | 9980 | |
| Db | 9599 | TCAGTAGACTATAATAATTAAGTTT | 9624 | |
| RESULT 11 | | | | |
| PPV | | | | |
| LOCUS | PPV | 9741 bp | RNA | linear |
| DEFINITION | Plum pox virus genomic RNA, complete genome. | | | VRL 22-NOV-1997 |
| ACCESSION | D13751 | D00424 | | |
| VERSION | D13751.1 | GI:222408 | | |
| KEYWORDS | complete genome; polyprotein. | | | |
| SOURCE | Plum pox virus | | | |
| ORGANISM | Plum pox virus | | | |
| REFERENCE | Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae; Potyvirus. | | | |
| AUTHORS | 1 (bases 1 to 9741) Maiss,E., Timpe,U., Brisse,A., Jekmann,W., Casper,R., Himmler,G., Matanovich,D. and Katinger,H.W. | | | |
| TITLE | The complete nucleotide sequence of plum pox virus RNA | | | |
| JOURNAL | J. Gen. Virol. 70 (Pt 3), 513-524 (1989) | | | |
| MEDLINE | 89279232 | | | |
| PUBMED | 2732699 | | | |
| COMMENT | cDNA prepared by primer extension was used to determine the 5' terminus. | | | |
| FEATURES | Location/Qualifiers | | | |
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D5 68 ATTCAAAGATTGGGGCGAGTTGGTCGAAACAAACCGAGGAGCAGCTTCGTATTGGATT 4757
QY 5257 ACAUUAAGGAUUAUAGAUUAUUGUGGCGACACAGCGUGCAUUAUUAUUAUUAUUAUUA 5316
D5 78 ACAGAGAAAGACTCACTCAATACCTCCATTAATCGCAACAGAGAGCTTTTCTATGT 4817
QY 5317 UUCACAUUAUGGUAUUGGUAUUGACAAAGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 5376
D5 88 TTCACTTATGTTTGGCCAGTATGACTAAACGGTGTGTCAACGAGCTTACTAGCGATGTG 4877
QY 5377 ACAGUCCGACAGCCAGAGUUAUUGUUCUUGUUGUUGGCGGUUAUUAUUAUUGGUUA 5436
D5 88 ACTGTCAAGCAAGCAGGAGATGCAACAGTTTGAATTTATCCCGTGTCTACACAGTGGG 4937
QY 5437 CUUGUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 5496
D5 98 TTGGTTGAGTTACGGGACATGCAACAGCAAGAAATTTTTCGATTGCTCAAGAGCTATAGA 4997
QY 5497 UUAAGAUUAUCUGAAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 5556
D5 98 CTGCGTGACTCAGAGTAACTTTAAACAAGTTGCTATACCAACAGCAAGCTATGTGG 5057
QY 5557 UGCGUAGUUGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 5616
D5 08 TGGTAGTGTTCGTGACTACAAACGACAGGCTGTAACCTTGACTTGGATGAAACATT 5117
QY 5617 AAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 5676
D5 18 CGTGTAACCGTTTACGTGAAGACATCCCTCGAAACTTTGACGAGAGAATATGGCAAGCG 5177
QY 5677 AUUCUCAAAUUAAGGACUAAAUUUGUUGUAGAUAGUUGUUAUUAUUAUUAUUAUUAUUA 5736
D5 78 GTAGAAACCCACAATCTGATCAGGATTCGGAAGGATCTGTAGTTCTGAGTGGCTGCAA 5237
QY 5737 GUAGCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 5796
D5 38 ATTCGCTATACGTATACAGACAGACATCCACTCCATTCCTCGGACAATTAATAATCATCGAC 5297
QY 5797 GCCUCUUGCAAGAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 5856
D5 98 GCAGTGTGGAGCAAGAGAAACAAGCAAGCACTTCAGAGCTATGACCACTCAATCC 5357
QY 5857 UGUAGUGGAAACAUUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 5916
D5 38 TGCTCAAGTTCAATTTCT 5417
QY 5917 AAGGACUACUCUGGCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 5976
D5 48 AAAGACCATACGGAAGAAACATTTGGTGTTCCTCAAAATGGCGAAGTCTCAGTTGCTAGAA 5477
QY 5977 UUCGUCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 6036
D5 78 TTCAAGAACCTGAACATTTGATCAAGTTATCTCTGAACTTATTCGCAACTTTTGGCGCTTA 5537
QY 6037 GAACAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 6096
D5 38 GAATGTGTGACCATCAAAACAAAGGAGGATTTCAAAGCGCTACAACTTAAGGGGCAT 5597
QY 6097 UGGAUUAAGUCACUAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 6156

D5 598 TGGAAATAAACGACTCATCTCGTGACGCAACATTAATGCTTTGGAGTTCTTGGTGAGGG 5657
QY 6157 UUCUGAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 6213
D5 58 GCATGGATGATTTTCAGTTTATTTGAGGATAGTTTCAAGAAGAGATTTATTCACCAAGGT 5717
QY 6214 -----AAGAGGAAGACUCAAAAGCUUAAUUCUGGAUGUCUGCGGAUAGAAAUUGGU 6267
D5 718 TTCAATCGTAGGCAAAAGACAAAATTTGAAATTTCAGGCAAGCCGAGATAACAGATGGCC 5777
QY 6268 CGAGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 6327
D5 78 AGGGAAGTGTATGGTGACGATTTCAACTATGAGGAGCATCTTTGGTTCTGCATCTCAAG 5837
QY 6328 AGAGUGGACUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 6387
D5 88 AAAGGAAGAGCAAAAGGAAGACTAGAGGATGGGACGAAACACGCAAAATTTGTGAAC 5897
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D5 88 ATGTACGGGTACGATCTCTACAGACTACAACCTTTGTTGCGCTTTGTTGATCCATTTGACTGT 5957
QY 6448 GCNAACGCGUAGAGAGUUCUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 6507
D5 98 CACACCTCGAGCAAGAGTCTCTTATGGACATCAACTTGGTGAGGAACACTTCTCGCAG 6017
QY 6508 AUCAGAGACAAAUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 6567
D5 08 ATTTCGATGATTAATCGAGATGACAAAATCAACATGACGACATATATGTAATTCATCC 6077
QY 6568 GGUUGACAGCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 6627
D5 08 GGTATTTGCGCATACTATATCAAGGATGCGACGAGAAAGCCCTCAAGTGGACCTCACT 6137
QY 6628 CCACACAAUCCUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 6687
D5 38 CCACACAAACCCATTCGCTGTATGTGACAAAACCTGCAAACTATTTGCGAGGATTTCCAGAGA 6197
QY 6688 GAGUUGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 6743
D5 98 GAGTTTGAATTCAGGAGAGAGACACCCAGCTTTTGTGTAACCTTAATGCAATCCCAAG 6257
QY 6744 -----AGAACGGAUAGACGCUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 6795
D5 28 ATCAATGAAGAGGGGACGGAAGATTGACACGAAAGTAAATCACTGTTTAGAGGCGCTG 6317
QY 6796 CCGAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 6855
D5 38 AGAGACTACAATTCCAATCGCAAGCTCGATATGCCAATTTGAATAACTCATCTCTGCTGCTAGA 6377
QY 6856 UCCACCACAACUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 6915
D5 78 CAAAGTGAATTTTGGACTTGGCTTTGGGGTTTAATTTGTCAGGATCAGCATTTGTTTC 6437
QY 6916 AAAGAAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 6975
D5 38 AAAAGGAATGACGAGAGCTAAATCCGATCCGATCATGGGGAATTCGTAGTGAAGGAC 6497
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D5 98 ACAAACACTCTCAAACTGCTTCTTTCGAAAGGTGGGACATAGTATCATCATGATTTACCA 6557
QY 7036 AAAGACUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 7095
D5 58 AAGGACTTCCCTCTTTCCGAGGAGGTTGAGTTCCGACACCCGACGACTGAGNACAGA 6617
QY 7096 AUUUGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 7155
D5 68 GTTTGTTTAAATTTGTTTCAAAATTTCCAAACGAAGAGCATTTCAAGCAACCATGTCGGAACA 6677
QY 7156 AGCAAAACUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 7215

Dd 3199 TTCTTCCAAAAGTTTTCAAGATGATGTGATATGCTAATTTGTGATCAGTCTTCTCTTGACTA 3258
Qy 3767 UUGGCAUUCAGCUAUUUAUUCGUUCGUAUGCAGUAUGCACAUAUAGAGAGAGAAAAGCAGG 3826
Dd 3259 TCGGTGCCACATGCAAAATCCAT--GATCAATGAGCATCAGCGCTCAAAACAGATGGCTG 3315
Qy 3827 UGAUAUUCGAGAAAGUUCUGAUAUAUUAUUGGCGCCUUAUAUAGGAGCAGAUAAAGA 3886
Dd 3316 TCGATCGTGAGAACAAATAAGAGGTTCAAGCGCTTTACAGCTTTTATATGCGAGGGTTACGG 3375
Qy 3887 UCAAUCCAG-----ACUCACAAAAGGAAGAAUUAUAGGAGUACAUUUGCAAGAAGUAGAC 3940
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Qy 3941 CUGAGCUUAUUGCAUUAUUAUAAAGAAUUGCAAGAA-----GAAGUUGAUCAUCAAG 3994
Dd 3436 CTGAACCTAGTTAAATATGCTGAGGACCTTATTGGAAGAGGTCAAGTTGTAGTCCATCAAA 3495
Qy 3995 CUAAAGCCAAAGGUGAACAACAAUUGGAGAAAUAUUAUGCAUUAUUGCCUUAUUAUGA 4054
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Dd 3556 TGTATTTTGATTCAGAGAGAGTGTATGGCGGTATACAGATTTTGACCAAGCTCAAGAGTG 3615
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Dd 3616 TCATGGGGACATTGTATCAAAACAGTGCATCATCAGAAATTTAGATGACATTTGAGGATATT 3675
Qy 4175 UGACUGACAAAGAAAACAACAUUGAUUUUGCAUUAUUGUAGUUGAGGGAGCAAAUUAUAC 4234
Dd 3676 TGGATGAGAGAAAGCTAAACAGTTGATTTTGTGCAAAAGTAATAGGTTGCAACCAACAG 3735
Qy 4235 AGUUAAGGAGUAGAAUUCUUGCCGCAUGUGGGAAGAAACAAUACUAUGUAGUAGAGUG 4294
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Qy 4295 UACCCCAUAUAGAAACACACUGGGAUAUUAUUGAAUUCACUCUGUAAAGCUGUUAUUG 4354
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Dd 3916 CAGGAAATCTACTGGCTACCACTTTCATTTGAGCAAAAAGGGTCAATGCTCTTACTTG 3975
Qy 4475 AACCAACAAGACCAUUGGCGAGAAUUGUCACGACAGUUGAGACAAUCCUUAUUG 4534
Dd 3976 AACCAACTCGACCATTTGGCTGAGATGTATGTAACAGTTGCGAGGACAACTTTCAATG 4035
Qy 4535 CAAACCCCAUUGAGAAUUGCGAGGAUUGUUAUUGUAGUUAUUAUUAUUAUUAU 4594
Dd 4036 TTAAACCCCAATTCGCGCATACGAGGGTTGACACTTTTGGCTCAACCCCAATCACTGTGA 4095
Qy 4595 UGACUAGUGUUAUUGCUUAUUAUUCUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 4654
Dd 4096 TGAAGTGGATATGACTGCATCTTTCTTGCAAAATATCCAGTTTACCTGGATAACTATA 4155
Qy 4655 AAUUGUGUAUAUAGAGUGUAGUGUAGUCCUUAUUAUAGCAACGCUAUGGCAUUCGUGUC 4714
Dd 4156 AATGCATCATTTTGGACGAGTGCAGGTTTCATGCGCATCCGCAATGGCAGTTAGATGTC 4215
Qy 4715 UUCUCAAAAGAACCAACUUAUUGGCAAAACUUAUUGAAAGUGUAGCCACCAACAGGGCC 4774
Dd 4216 TGTATCGGAATACTCTCATCCAGGGGAAATTTCTGAAAGTCTCAGCGCACCTCTCTGGGC 4275
Qy 4775 GUCAUUGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 4834
Dd 4276 ATGAGGTGGATTTCAAGACACAAAGGAAGTCAAGGTCTATGTCGAGGAATCATTTGTCAT 4335

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Dd 4336 TCCAACAATTCGTGTCAAAATCTTGGGTCTGGTTGCAACAGTATATCTTTGAAATATGGCG 4395
Qy 4895 ACAACAUUUUAGUGUAUUGCUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 4954
Dd 4396 CAAACATCTTGTGTACGTAGCAAGTTAATGAAGTTTGAAGTTCGAAAGCTTCTCA 4455
Qy 4955 GAGUAAAAGCGUAUUUAGUAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 5014
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Dd 4516 AGATACCAACGAGCGCGCAGCAAGCTTAAGCCACATTTCTGTTGGTTCGCAACAACATTA 4575
Qy 5075 AGAAUGGAGUCACUCUAGUAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 5134
Dd 4576 AAAATGGTGTACATTTGGATATAGATTTGTTGTGACTTCGGGTTGAAGTGGTCCCTG 4635
Qy 5135 AAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 5194
Dd 4636 TTCTAGACGTTGATTAATCGGCTTGTGCGGTATACAAAGACAAGTATCAGTTATGGCGAGC 4695
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Dd 4696 GGAATTCAGCGACTCGGTGCTGTTGGTTCGAAACAAACACGCGCGCAGCATTTGCGAA 4755
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Dd 4756 TCACAGAGAAAGGTTTAAACACAGATTTCCACCAATGATTTGCACTGAGCGCGCTTTCT 4815
Qy 5315 GCUUACAUAUUAAGAUUUGCUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 5374
Dd 4816 GCTTACATATGTCTCCCTGTCATGACAAATGGTGTATCGACAGCTTCTCGCATGT 4875
Qy 5375 GCACAGUCCGACAGCCAGAGUUAUUGUUCUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 5434
Dd 4876 GCACGCGTGAAGCAGCGCAGCACTATGACAGCTTCGAACTGCTCCCTTTCTACACAGCAG 4935
Qy 5435 CACUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 5494
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Qy 5495 AGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 5554
Dd 4996 GGTGCGGACTCAGAAAGTGTCTTGAATAGTTGGCCATACCAATGCGAATGTTGGTG 5055
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Dd 5056 GGTGGATGAGCGTGCAGATTTACAAAGCGCAAGGCTGTAATTTGGATCTTGACGACAATG 5115
Qy 5615 CAAAUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 5674
Dd 5116 TTGCGATTCATCTCACTGCAAGGATTTGCTGAGCTTTTGCATGAAACATATGCAAG 5175
Qy 5675 AUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 5734
Dd 5176 CGTTGAGAAATTTACAAATCGGATGCTGGTTTGGTAGGATTTGTAGCTCTAGTGTGCA 5235
Qy 5735 AAGUAGCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 5794
Dd 5236 AAATAGCTTACACATGACGAGCGGACATACACTCCACGAACTGTCAAAATCATTTG 5295
Qy 5795 AGCCCUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 5854
Dd 5296 ATGTATTTGTAACAAGAGCGGACGAAACAGGCTCATTTTATGGGCTATGACAAAGTCA 5355
Qy 5855 CAUGUAGUGGGAACACUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 5914
Dd 5356 CATGCTCAAGTTCAAAATTTCTCTTGTCCAGTATTACATCAGCCATTCATCGAAGTACG 5415

QY 5915 CUAAGACUACACUGUGGCAUAUUCAGAAAUUGCAGGACGACAAAGAAUCAAUACUGG 5974
Db 5416 CGBAAGATCATACAGAGGAGATATTGGAGTGCCTTCAATATGCAAGGCGCAACTCTTAG 5475
QY 5975 AAUUCGUCAUUUAUUAUUCUUGAUUUCUGGCGAUAUCCGGAUUCUUAAGAGUUCGAGCUU 6034
Db 5476 AGTTCCAAAACATTGAACATTGTATCCCAAGCTATCCCGAACTTGTGCGCAACTTTGGTGCA 5535
QY 6035 UAGAACUAGUACCCCAUCAGACGAGCAGCAAGAAUUAUUAUUAUUAUUAUUAUUAUUAUUA 6094
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QY 6155 GUUUCUGGAGUAUUAUGGGAUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 6214
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QY 6215 AGA-----GGAGACUCBAAGACUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 6265
Db 5716 GGTTCATCGACGGCAGACAAAACCTTAAGTTTCGCCAAGCTCGCGATNACCGGATGG 5775
QY 6266 GUCCGAAGUAUUAUGGAGACGCGUAUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 6325
Db 5776 CCCGAGAAGTGATGGAGATGATTCACGATGGAGAAATATTTGGTTCAGCATACTCA 5835
QY 6326 AGAGAGGUCAGUUAAGGCGCAGAGAGAGGAAUUGGCGGAAAAUUAUUAUUAUUAUUAUUA 6385
Db 5836 AGAAGGCGCAAAAGCAAGGCTCGACACAGAGGATGGGCAACCAAGACGAGAAAGTTTCTGA 5895
QY 6386 GUUAUUAUGGUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 6445
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QY 6446 GAGCAACGCGUAUGAGAGUCCUUUAGACAGAUUGGAAUUAUUAUUAUUAUUAUUAUUAUUA 6505
Db 5956 GGCATACACTCGATGAGATCTCTCATGATATAGTTTGGTGCAAGCACTTCTTA 6015
QY 6506 AAUUCAGACAAAAUUGCUAGACGAGGCGCUCAUGAUUAGGCAACAUAUUAUUAUUAUUA 6565
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QY 6686 AGGAGUUGUUGGCAAAACGGAACAAAGCAUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 6745
Db 6196 GAGAGTTGAGTTGAGACAAACAGGACAGCCAACTTTCGTAACCCAGCGCTGTGCCAA 6255
QY 6746 AACGGAUUAAGC-----UUUUUUUAAGGAGCCUUAUGUUAUUAUUAUUAUUAUUAUUA 6793
Db 6256 AGGCAATGAGTGTGAGGTGAGGAGTGCATCATGAAGCAAGTCACTATTAGAGTT 6315
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QY 6914 UUAAGAAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 6973
Db 6436 TTAAGAGGAATGACGGAGAGTTGACAAATTCGATCACACCAGGAGGATTTGTTCAGGG 6495
QY 6974 ACUCCAAGCAAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 7033

Db 6496 ACACGAAAACACGCAAAATTGCTGCCTTGAAGGTCGGGACATTGTGATCATCAGACTAC 6555
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Db 6616 GGGTTTGTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 6675
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QY 7333 --GGCGAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 7390
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Db 7033 CAACGCACTGGTTACGCAAGCTTGAAGGCAATTTGAAGCGGTTGAGCGCTGTCCAG 7092
QY 7571 AUAUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 7630
Db 7093 GACAGCTGTTTACGAAGCACGTAAGTGAAGGGAATGACACACTGTTTCGAAACCTACTTGC 7152
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Db 7213 CTCTAAATAAGGATGCTACGTAAGGATCTGATGAAGTATTTCCAAGCCCATAGTTGTTG 7272
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QY 7811 AAUGGAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 7870
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Db 7453 TGTCTGAAAGATGAAATAATGAATTTGTGCGTGGCAGCTGTAGACGTCTATTATTTGGGCG 7512
QY 7991 AUUUGGAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 8050
Db 7513 AGAAGGAGTCTGGAAACGATCACTCAAAAGCTGAGTTGCGACCAAGAGAAAGTTCGAAG 7572
QY 8051 CAAAACAAACCGCAACUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 8110

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| 7573 | CTAACA AAAACCGCGCTCATTCA CGCGCAGCAGCCCACTTCTTCGCGAGGTAAGTGT | 7633 |
| 8111 | CGCUGCGAUGAUUUUCAAACAACAAUUUUUAUGAUUUUAUUAUAAUAGAAUAGCCCAUGGACAGUCG | 8170 |
| 7633 | CGGTAGACGACTTCAACAATCAGTTTTACAGCTGAATTTACAGCTGCTCTTGAGTGTTC | 7692 |
| 8171 | GGAUGACUAGUUUUUUGCGGAUGGAAUGAUCUUUUAUGGUAAACUUCUUGAUGUUUGGA | 8230 |
| 7693 | GAATGACAAAATTCAGAGGTGGATGGGACAAGCTGCTTAAGGTCGTTGCCAGATGGCTGGA | 7752 |
| 8231 | UAUACCGCGAUGUGACGGAUGAUUGACAGUUCUUIUACACAUACUUGUGAAUG | 8290 |
| 7753 | TTTATGTGATGCGGATGGCTCAAAATTTGATAGTCTCTTGTACCATACTCTCAATTAAG | 7812 |
| 8291 | CAGUGCUGGGAUUAAGGAGUUUUUAUGGAAUGGGAUAGGCGUGGCAUGAUGCUUC | 8350 |
| 7813 | CAGTCTGMACTTCGGTTAGCTTTTCATGGAAAAATGGGACATTTGGTGAACAAATGTTAT | 7872 |
| 8351 | GAUAUUUGCACUGUAAUAUAUUUUAACACCCCAUUGCAACACCUUGAUGGAAACAGUCGUCA | 8410 |
| 7873 | CCAACTTTGTACACCGAGATTGTTTACACACCAATAGCAACCCCGGACGGAAACCACTGTCA | 7932 |
| 8411 | AAAAGUUUGAGGAAUAUAGUGGUCAAACCGUCAAACAGUCGUAGUAUAACAUUGAUGG | 8470 |
| 7933 | AGAAAGTTCAAAGGAAATTAATGTGGGACAAACATCCACAGTCGTAGTAATACCGTCAATGG | 7992 |
| 8471 | UCUGAUUUUGUGCAGUAGUUAUUUAUUAUAGUUAAGUUAAGUUUGAUAUCAGGAUG | 8530 |
| 7993 | TCATTTAGCAATGACATACCTCGCTTTTGAAGCTTGGATACCATCCAGACACACACGACT | 8052 |
| 8531 | AUGUCUGAGGUAUUUCGUUAACCGGUAUGAUUUUUGUUCUUAUACAUUCCAAAAUUUA | 8590 |
| 8053 | GTATTTGCAAGTACTTTGTGTAATGGTGATGACTTAGTTATAGCGGTTCACTCCGTCGCATG | 8112 |
| 8591 | UACACAUCCUAGAUUUUUUAAAGUUAUUUGCUAAUUUAGUUUAGUAUAUUAUUCU | 8650 |
| 8113 | AGCACATTTATGATGAGCTTCAAGAGTTATTTTCCAGCTCGGATTTGAACATCACATTTCA | 8172 |
| 8651 | CUCAUCCAAACGAAAGACAAAGGAGAAAUUUGUUUAUUGUCUCAAAAGGAGUUAUUAUA | 8710 |
| 8173 | CAGCGAAAACCGAGAAACAAAGAGAGCTATGGTTCATGCTCTCAAAAGGTGATTGCATG | 8232 |
| 8711 | AUGACUUAUUAUUCCAAAGCUGAGCCAGAGAGGUGUUCUUAUAUUAUUGUGGUAUA | 8770 |
| 8233 | ATGGGATGTATCTCCGAAGTTGGAACTCGAAAGGATAGTGTCAATCTTGTAGTGGGATA | 8292 |
| 8771 | GAAGUUAUAACACAGAACACAGAUUAGACGGAUUUGCGUUGAUGAUUAUGAAGCAUGG | 8830 |
| 8293 | GGTCACATGAACCAATTTACAGATTTGGAAGCAATTTGTGTCATCGATGGTTTGAAGCTTGGG | 8352 |
| 8831 | GUUACCCUAGGUUAUUCACGAAAUUCGAAAUUUUAUUGUCUGGUGUUCGGAACAAGCAC | 8890 |
| 8353 | GTTATGAGATCTGTTGATGGAAATTCGAAAAATTTTATAGCTGGTCTTTGAAACAGCAC | 8412 |
| 8891 | CAUACAUAUCUCGCAUCUGAGGGAAGGCACCAUAUAUUUGGAAACACGCGCUCAAAA | 8950 |
| 8413 | CGTACAATGCCCTCTCGAAAGATGGAAGAGCTCCATACATAGCAGAGACTGCTCTGAAA | 8472 |
| 8951 | GACUUUAACAUUGCGAAGAGGAAGUCUGAUGAAUAUCAUUAUUAUUAUUAUUAUUGUG | 9010 |
| 8473 | AGTTGTACACAGATGAAGAAGCTTCTGAGACAGAGATTGAGAAATACCTTTGAAGCCCTTCT | 8532 |
| 9011 | CAAGUGAU-----UUGAACGAGGAUGAGUACUUG | 9040 |
| 8533 | ATAACAATGTGGGGATGAGCTCGATTTCCAAACATAGTGGTGGCATCGAGCCACAGGAGAA | 8592 |
| 9041 | AUGAUGAAGAUUUUUCACACGAGCUCUCUUGAUGUCUGGCAAAACCCACAGCAGAAAAACA | 9100 |
| 8593 | ATGATGACGGGTAACTCTAGTGGATGACGGCAAGTCTACTGTCAACACACAGCAGTTTCCA | 8652 |
| 9101 | AGAAAGACG----- | 9109 |
| 8653 | CGCCTGCAGTAAACAAGCTCAAAATTTCCACTCCACCATTTCCTCCAGATCTCGAGACGCG | 8712 |

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| Qy | 9110 | -----AUGAAGAGAGAAAGAAUAAAGAAAGACGAGGAAAUAAAGAAACAAAGAAUA | 9160 |
| Db | 8713 | CACCAATGTTTGATCCATATTCACCTCCAGCAACACCCAGCCAAATGTGAGACCGATTG | 8772 |
| Qy | 9161 | AAGAAGUCGAGAGAAAC-----AUGAAGAAACUUCGAAUAGCG | 9199 |
| Db | 8773 | CACCAAGTAGTGAACAAGTCCATTCCTGATGGGGTAATTTGGGAACCGAAGACGTGACACCTT | 8832 |
| Qy | 9200 | CAUCUGUGCUAUUUUUUCAAACAACAGAAAGAAAGCAAGGAUGUCGUAUGAAGGAUCAAAGUG | 9259 |
| Db | 8833 | CCTCTCTCAATGCACCTAGTCAACACGAGGAGAGATCGAGACGTAGATGCAGGAACCGATTG | 8892 |
| Qy | 9260 | GAUCUUUUAUCAUACCAACGAAUUAAUUCGAUUAUCCAAUAAACUCAAAUUGCCAAAAAGUGA | 9319 |
| Db | 8893 | GGACCTTCTCCGTACCTCGACTTAAGTCTATGACTTATGAAATTTATCACTCCCAAGGTGA | 8952 |
| Qy | 9320 | AAGGGAAAGAAUUUUAUUUUUAGGAGUUCUUUUUACAUAACACACAGACAUAAGUGGACA | 9379 |
| Db | 8953 | GAGGGAAGGCCATCATGAACCTCAGTCATTTGGCTCATTTATATCTCGCAACAATGACT | 9012 |
| Qy | 9380 | UUUCAAAUACCGGGCAAGUUUUCACAGUUUAAUACAUGGUACAACCGUGUAGGAAGAU | 9439 |
| Db | 9013 | TATCAAAACCGGGCTCCTCAATCTGTTTCCAACTTGGTATGAAGAGTCAAGCGAG | 9072 |
| Qy | 9440 | CCUAUGGUGUGUCUGAUGAAGAAUUGGGAUAUAUUUUUGAAUUGGAUUAAUUGUUUUGUGUA | 9499 |
| Db | 9073 | ACTACGATGTTTCGGATGATGAGATGAGCATCATTTTGAATGTTTATGATGTTGTTGTTGCA | 9132 |
| Qy | 9500 | UUGAAAUAUGAACAUCUCUCAAACAUAUUAUGGCAUGGUUUUAUGAUGCAAGGGGAAGAAC | 9559 |
| Db | 9133 | TTGAAATGTGAACCTCTCAAAACATCAATGGGATGTGGGTATGATGGATGGAGAGACAC | 9192 |
| Qy | 9560 | AAAUCAAUAACCCCUCAACCAUAUAGGAAACGCAAAACCCCAUUCGUGUCAGAUUA | 9619 |
| Db | 9193 | AGTGGAGTATCCAAATAAAGCCATTGTTGGATCATCGGAAACCCACTTTTATGACAAATTA | 9252 |
| Qy | 9620 | UGGCUCACUUTUAGCAUUGUCUGAAGCAUAUCAUCGAAAGAGAAUAUUGAAGACCCAU | 9679 |
| Db | 9253 | TGSCACATTTACGTACGCTGCTGAAGCGTATATTGAAAGCGGAACCTATGAGAAAGCAT | 9312 |
| Qy | 9680 | AUAUGCCGAGUACGGUUAUUAACCGAAACUACACCGACAUGAGUUUGGCGCAUAGUUU | 9739 |
| Db | 9313 | ACATGCGAAGGTATGAAATTCAGCTCAACGTGACAGACTACAGCCTCGCCAGATATGCGCT | 9372 |
| Qy | 9740 | UUCAUUUUAUGAAUAGCAUCAAGGACCGCAGCUCGGGCCCGGGAAGCCCAUCCAGA | 9799 |
| Db | 9373 | TTGATTTACAGAGATGACCTCGAACCGCTGTGAGGGCTCTGTAGGACACATATTCAA | 9432 |
| Qy | 9800 | UGAAAGCUGCAGCAUUGCGAGAUUGCAUUAUAAUGAUUUUGGACUGGAGUAAAAAGUCG | 9859 |
| Db | 9433 | TGAAGGCAGCAGATTGAGAAATGTTCAAAATCGTTTATTTGCTTGGATGGAACGTCG | 9492 |
| Qy | 9860 | GAUAUUGCAGUGAGAACACGGAGCGCCACACCGCAGACGAUGUUUAACCAUACACUUAUG | 9919 |
| Db | 9493 | AAACACAAGAAGAGGACACAGAGAGGCACACCGCTGGTATGTTAATCGCAACATGCACA | 9552 |
| Qy | 9920 | CAUUCACCGGCUUCCAUUAUUUAGAUUUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU | 9974 |
| Db | 9553 | ACCTCTCGGTGTGGGGGAGTGTAGTGTCTCGGTATCCATCATATAAATCTACT | 9607 |
| RESULT 13 | | | |
| AB093602 | | | |
| LOCUS | AB093602 9798 bp RNA linear VRL 23-JUL-2003 | | |
| DEFINITION | Turnip mosaic virus gene for polyprotein, complete cds, | | |
| | isolate:ISI. | | |
| ACCESSION | AB093602 | | |
| VERSION | AB093602.1 GI:33146230 | | |
| KEYWORDS | Turnip mosaic virus | | |
| SOURCE | Turnip mosaic virus | | |
| ORGANISM | Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae; | | |

Db 1155 TGATGCCATAAGATTGTGCACCTTTAGTCGGCAGGAAACAACTCTCTGGAAGGCTTTG 1214
Qy 1610 AUCGUCAUUUAUUGCAUUCGAGAUAGACUUAAGAAACGCUCAUGUGCAAGGCCCAUA 1669
Db 1215 ACAGATGCTTTCTAGCATACCGCAGTAACGATCG- --AGAACAACATGTTTACACAGGAC 1271
Qy 1670 UAAACGUUGAGGAGUGUGGCGAAUUGGACGCAUUGUAACCAACUCCUUAUUCCAUGU 1729
Db 1272 TTGATGTCACTGAGTCGGGAGAGTAGCAGCTTTGTGTGTCTTGTGCAATGTTCCCTCGC 1331
Qy 1730 GGAUUUAUACAUCAUGCAUUGUGGAGAAACUGUUGAAUUGUUGUCAACAAGAGAGGAAC 1789
Db 1332 GAAUAATAACCTGCCCTGCTGTGTACCGATAGCGAGTTGGTCAAGGCCAGGCAAGTG 1391
Qy 1790 UUGAAUUCUUCAGGCGUAAAGAGGCCAAUUGGCAAGUAAUUAUCCAGUCUUAUUAUCA 1849
Db 1392 CACCTAATAAACAACAGATTGGCCCAACTGAGGGAAGTGAATTAAGTCAAGTTATCCGC 1451
Qy 1850 AUUUUCCUAGUGGUAUUAUUAUUGAUAUGAUAUGAUAUGUCUGAAUCGGAUGNACA 1909
Db 1452 GGTTTAAACACGCGAGTCGAGATCTGACAGGATGAACAATCACTCAATGGTGAACAACG 1511
Qy 1910 CAAACUUCGAGCGCAACAAUUGCAACAAUUAUUGGAGUCGCGCAAGAGAUUCCU 1969
Db 1512 CAATATACAGACTTCGAGAGATTCAGAGTCTGACTGATGATGATGGAAGAGCAGCGT 1571
Qy 1970 UUUCAAUUUAGAGACUUCGUAUGAAUUGCUAUAUUAAGUCGGAUAAACUUUUGAGCGAG 2029
Db 1572 TTCACATGCGAATAAATTGAACGCCATAATTAATCAAGAGAGCTACGGCAACAGCGGAGG 1631
Qy 2030 AUUUCUAUGAAUUGUUCUAUGCCUUUUAAGCUUAACACGUCGCAUUAUAAACAGGAGCG 2089
Db 1632 AGTATGAACAGCAACAAAGCACTTGTAGAAATCACCCGATATATGAAGAACCGCACTG 1691
Qy 2090 AUUCAUUAAGAGGAGAGAUUACCAUUAUUGGAAUAUAGUUGACAGGUAAGCACAU 2149
Db 1692 ARAACATTGAAGGGATCACTTAATCCTTTGAATAATAGATATCCAGAGGCACACA 1751
Qy 2150 UUAUUUUUGCAUUGUGUGACAAACCAACUUGCAAAAAUUGGUAACUUCUGUGUGGGUG 2209
Db 1752 TCAATCCAACTAATATGTGTGATAATCAACTCGATAAGATGCAACTTCATATGGGTG 1811
Qy 2210 AAAGAGUUAUCAUGCGAAGAGUUUUUUAACUUCUUAUGAAGAAUGUUAUUCACUG 2269
Db 1812 AGCGAGGTTATCATGCGAAGAGATTCTTTAGCAATTAATTTGGAATAATTTGACCCAAAGA 1871
Qy 2270 ACGGUUAAGAAACACAUAUUGCGAGUCAACCAACCAUUGGCAACAAACAGCUAUG 2329
Db 1872 AAGTTACACCCAGTAGCAAACTAGATAAGTACAAACGGTTCTAGAAAACCTCGCTATTG 1931
Qy 2330 GAAAAUCGUUUUAUCGACGGAUCCAUACGCUACGACAAACAAUUGAAGAGUAGCCCAA 2389
Db 1932 GTAAGCTCATAGTCCCGACAAACTTTGAAGTCTTGAGAGAGCAGATGAGAGGGGAACCTG 1991
Qy 2390 UCACAGAGUUCAGAUUGGUUAUUAUUGUAACAGCAAAAGAGAGUUGUUAUCGUUAUC 2449
Db 1992 TAGATCCACATCCAATCACGGTGGAGTGTGTGAGTAAGTCACAAGGTGACTTCGTTCAAG 2051
Qy 2450 CAGCAUCGUGUUAACAUGGAAGAGUAGCGCAUUGUUUUUUGUUAUUAUUAUUAUUAUUA 2509
Db 2052 CATGTTGTCGGTAACACTCTGAGTCAGGTGATCAGTATTGTCGTAATCAAAATGCCAA 2111
Qy 2510 CUAGAUAUCAUAGUUAUUGGAAAUUCAGGAGAUCCAAAGUAUUGGUAUUAACCAAGCA 2569
Db 2112 CGAAACACCACTTAGTGATCGGAAATAGTGTGATCCAAATATGTTGATCTTCCAGAGA 2171
Qy 2570 GCUCAAGUGACAUUAU- --UGUGGCUAAGGAAGUUUAUUGUUAUUCUUAUUAUUAUUA 2626
Db 2172 TTGAAGAGAAACAAAATGATCATAGCCAAAGGAGGCTACTGCTATATCAACATATCCTCG 2231
Qy 2627 CAUUGUUGUUAUGAUGAGAGUAGAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 2686
Db 2232 CAATGCTCGTGAACGTCAGAGAGTCAACAGGCAAAAGAAATTCACCAAGAGTTGTTAGAGACA 2291

Qy 2687 UAAUUGUACCGCGUCUGGUCUAAUGCCAAAGCUUAUUAUCGAUUGUUGCAACUGAAUUGUACU 2746
Db 2292 AATTGGTTGGTGAACCTAGGCAAAATGCCATCGTGTGTAGATGTTGCAACAGCTGTTATT 2351
Qy 2747 UCCUUAUCGCCUUCACCCUGAAGAAACGAAAUUUGUGUGGUGCCGAAUUAUUAUGAGUAC 2806
Db 2352 TCTTGAAGAGTCTTTTACCCAGAGCTCGCTAATCCGAATTTACCAAGATGCTGGTGATC 2411
Qy 2807 AUAACAUAUAUUGUUGAUGUAGUAGUUAUUAUGGCGUAGACACCAACAAUUAUUAUG 2866
Db 2412 ACAAACGAGATAATTCATGTTGTGCACTCATATGGTCAATTTCAACGGGATACCA 2471
Qy 2867 UUCUGAAGGCAAAUACUGUAAGUCGUAUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 2926
Db 2472 TCTTGAAGACGAAACACAGTTGAGCAACTATCAAGTTTACAGACACAATCTTGAATCAA 2531
Qy 2927 AGCUGAAACAUUAUUAUUAUGAGUGGA- -----GACCUCAUAGCA 2965
Db 2532 GCTTAAAGCACTACCCGCTTGGCGGCACGAAATGGGAGGATCTCACGGAGCCAGGAACA 2991
Qy 2966 AGCAAGCUCUCAGUGUUCUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3025
Db 2592 TTGATGATCCACAAATGGTGCATCAACAGACTCTGTGAAGAGGATATACAGACCAACAAT 2651
Qy 3026 UGAGGCAUUGCAUUGAGGAGAGCCUUUUUUUGUUAUUAUUAUUAUUAUUAUUAUUAUUA 3085
Db 2652 TAAAGGAAGACATGTTGGCAAACTCTTCTGTCACATATACGCCCTACTTTTCAACCAGGAG 2711
Qy 3086 UUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3145
Db 2712 TAATTTTGGCTTCTCAATAGTGGTTCGCTAGAATATTTGTGTAACCATTTATCATCAGAG 2771
Qy 3146 AGCAACAGUCUGUGCGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3205
Db 2772 CAGACAGCAATGTCGGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 2831
Qy 3206 UUGCUCAAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 3265
Db 2832 CAAGCCAGAGTGTATTGGTCAACTCCAGTCAATTGAGAGAAGCTTACCGAGCTTGTGG 2891
Qy 3266 CGGUCAUGAAGAACCAUUAACACAGACAGCAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3325
Db 2892 AAGCTAGAGCTAACATTACTGGATCAGAGGTCGGCATCTCAAGCATGTAAACAGATTC 2951
Qy 3326 AGGUAUGGCAAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3385
Db 2952 TTGGCATGTTTATCATAGTTCGGAACCGAATTAATGAGCTTTTAGATGGTGATACAA 3011
Qy 3386 UACAAUCUGAAGUAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3445
Db 3012 CTTTGGGAGATCATAGCATAGCCATACTGGAATAAAAGCTATCTGCAAACTCTTGGACGA 3071
Qy 3446 CGUGGAACCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3505
Db 3072 CATGGAGAGTAAAGCTGTTGGAGCGTGTGTGTAAGATACTACTCTGCTAAAGCAAG 3131
Qy 3506 CAAUUAUCUGGAUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 3565
Db 3132 CAATCTTTTCACAGAAAGATTTGCCCATGCAAGCGACGTAGATTATTAGGCGGACATACA 3191
Qy 3566 CAGUAUUCGAAAGCAGUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3625
Db 3192 GCGAGTCGTCATATCTCTCCTAGAGTGGGTAAAGCAGCGTATGAAGAAACTTTTACTCTG 3251
Qy 3626 AAGCAAGAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3685
Db 3252 GCTGTGCAACAAACACGCAATAGCATGCTCTGTGTAGTAGGAAGTCTCTAGTGGCG 3311
Qy 3686 CAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3745
Db 3312 TTTGTAGAACTATTAAATTAACCTAGTACCAGATATTTTATAGTTTATTAACGTTTAATTT 3371

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| QY | 3746 | UUUAUAGUUUAUUCUCAGCAUUGGCAUUCAGCUAAUUCUUAUAUCGUUCGACUUAUGCAC | 3801 |
| DB | 3372 | GTATTAGTTTGTACTCAATAGTCTTGAGACGTAATCGTATTGTTCACAGCGCAAGAA | 3431 |
| QY | 3806 | AAAUAGAGAGAGA---AAACGACGGUAAUUCGAGAAAGUUCUGAUAUAUUUAGUGG | 3862 |
| DB | 3432 | GGCTTAAGCTAGACGTCGTGGAGCGGAACGTAAAGAGATAGAAATGGGAACCTTGCAATTCC | 3491 |
| QY | 3863 | CCUUCUAUAGGAGCAGAUAAAGAUCAUUCAGACGUCGACAAAGAGAAAGAUUAUAGGAGU | 3922 |
| DB | 3492 | ACCACTCTATTTTAACCTCATAGCCCAATCAACATCCGACATTCGATGAGTTGCAGAGT | 3551 |
| QY | 3923 | ACAUUGCAAGAAGUAGACCGUGAGCUGAUUGCAUUAUUAUAAAGAAUUCAGAAAGAAG | 3982 |
| DB | 3552 | ACATCAGTCGGAAGACCCCATCTCAGTGAGTACATCGAACCTGAA--GAAAGGGAAG | 3608 |
| QY | 3983 | UUGAUCUAACGUAAGCGCAAGGUGAAACAAACUUGGAGAAAUUAUAGCAUUAUUG | 4042 |
| DB | 3609 | TAGTACATCAAGCAAGAGGCGAGTCTGCAACAAGAGCTTGAACGAATCATAGCTTTTATAG | 3668 |
| QY | 4043 | CCUUAUUUAUGCAUUAUUUCUCAGAGAAAGUAGUUGUUAUUAAGACACUCUGAACA | 4102 |
| DB | 3669 | CTCTAGTACTTATGATGTTTGATCGAGCGGAGTGATTTGGTTACAAAGATTCTCAATA | 3728 |
| QY | 4103 | AAUUGCGAAUUCUGUUGCCACAUGUGAUGAACCGUCGACCAUCAUAAGCUUGAGCGACA | 4162 |
| DB | 3729 | AGCTAAAGGATTAGTTTCCACTGTGGAAACCCACAGTGATCATCAAGCACTCAACGACA | 3788 |
| QY | 4163 | UUCAAAGACUUCUGACUGACAAGAAACAACCAUUGAUUUGCAUUAUUGUAGUGGGGA | 4222 |
| DB | 3789 | TTGAAGATGATTTGAGTGAGAGAAATCTCTTTTGTGACTTTTGAACCTCAGCAGTGACGGCG | 3848 |
| QY | 4223 | GCAAGUUAACAGAGUU--CAAGGAGUAAGUAUUUGCGCAUGGUGGGAAGAAACAACUAC | 4279 |
| DB | 3849 | AGTAGTCCAAAGCTTCCAGCTGAAAGACATTTGTCATGTTGGTGAACCATCAATTAA | 3908 |
| QY | 4280 | AAUGUGAUGAGUGUGUACCCCAUUAUAGAAACCAUGGGAAAUUAUUGAAUUCACUCUG | 4339 |
| DB | 3909 | GTAGGGGATACAAATCCCACACTATAGAACAGAGGGAAGTTTATGACTTTTACCAGAG | 3968 |
| QY | 4340 | AAAGCUGUUAUGUGUGAGUUAACAUAUUCUAUGCCCCUGAGAAAGAAUUGGAUAGUCC | 4399 |
| DB | 3969 | CAACAGCAACACAGATTTCGGCGCAGGATAGCACATGAGAGTGATAAGGATATACTGCTTA | 4028 |
| QY | 4400 | GUGGUGGUUGUACGAGGAUUAUCUACUGUACCAUUCGCGGUUAUCUAGUAUAAAGCGG | 4459 |
| DB | 4029 | TGGGAGCAGTGGGATCAGGGAATCAACTGTGCTGCGGTATCATCTCTAGGAAGGGGA | 4088 |
| QY | 4460 | CAGUUCUUAUGCUCGCAACCAAGACCAUUGGCGAGAAUGUCUCACGACGAGUUGAGAC | 4519 |
| DB | 4089 | ATGTGTACTGCTCGAACCACTCGACCACTTGACAGAAATGTCCATAAGCAGCTTTCAC | 4148 |
| QY | 4520 | AACAUCCUUUAUUGCAAAACCCACAUUGAGAAUGCGAGGAUUGUCAUCUUUUGAUCUA | 4579 |
| DB | 4149 | AAGCCCGCTTCCACCAAAATACAACCTCTGAGAATGCGGGGATTGACAGCATTTGGCTCGG | 4208 |
| QY | 4580 | GUAAUUAUUGUAUAUGACUAGUGUAUUUGCUUUAUUAUUCGAAAUUAUCCUCUAA | 4639 |
| DB | 4209 | CACCAATATCATGTATGACGAGTGGTTTGCACTTAACCTACTTCGCAAAATAACAGAGCAC | 4268 |
| QY | 4640 | AAUUAUGUAUUUUGAAUUUUGUAUAUAGUAGUGUACGUCGUUAUAGCAACGCUA | 4699 |
| DB | 4269 | GAATTGAAGAAATTGACTTTTGTATATTTGACGAGTGCACGTTCTATGACGCCATGCTA | 4328 |
| QY | 4700 | UGGCAUUCUGUGUUCUCUCAAAGAAACAACAUAUGAUGGCAACUAUUGAAAGUGUCAG | 4759 |
| DB | 4329 | TGGCGATGAGGTGTCTACTACAGATTGCGATTACTCCGGCAAGATTATTAAAGTATCAG | 4388 |
| QY | 4760 | CCACACCAACAGGGCGUAGUAUUCACACACAGCAUCCAGUUAUUAUUAUUAUAG | 4819 |
| DB | 4389 | CAACACCAACAGGGCGAGGTTGAAATTCCTCACTCAGTACCCCTGTAAACAAATAGCACAG | 4448 |
| QY | 4820 | AGGAACACUUAUUUUCAAAGCUUUUUGUAAGUAGUAGUACGUCGUUAUAGCAAGUAG | 4879 |

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| Db | 4449 | AAGACACATTGTGCTTTCAAAATTTTGTGAGTCGCAAGGTAGTGGGAGCAATTTGTGATG | 4508 |
| Qy | 4880 | UAAUCAUAUAGGAGAGCAACAUAUUUAGUGUAUUGUCUAGUUAACAAGAGGUUGAUCAGC | 4939 |
| Db | 4509 | TGATTTCAAAGAGAGATACATCTACTGCTGTCGTCGTCGCAAGCTACACGAGGTGGACAC | 4568 |
| Qy | 4940 | UCUCAAAAAUGCUCGGAGUAAAAGGCUAUUUUAGUGACAUAAGUCGUAUGGCGUACAUGA | 4999 |
| Db | 4569 | TTTTCAAGCTTTTGGCTGAGAGAGATTTTAAAGGTCACAAGAGTTGATGGGAGACAATGA | 4628 |
| Qy | 5000 | AAUUGGUCGACGCAUAUUAUAAGGAGUAGCCAGAGAAACAUAUUAUUAUUAUUAUUAU | 5059 |
| Db | 4629 | AGGTTGGGAACTTGAATTAACGACGAGTGGAACTCCACGACAAGAGCATTTTCATAGTTG | 4688 |
| Qy | 5060 | CAACCAAAUAUUCGAGAAUGGAGUACUCUAGAUAGUAGUUGUUGUGGACUUUGGUU | 5119 |
| Db | 4689 | CACCAACATCATTTAGNATGGTGTACTTTGGACATCGATGTAGTTGCTGACTTTGGAA | 4748 |
| Qy | 5120 | UGAAAGUCACUGCUGAAAUAUUAUACACAACCGGUGCUUAAUUAACAAGACACGACGA | 5179 |
| Db | 4749 | CAAAAGTACTTCGCTACCTTGACACAGATATAGAAATGCTTTAGCACGACAAAAGTAAGCA | 4808 |
| Qy | 5180 | UUUCAUAUCGAGAAACGCAUAACAAGAUUGGCGAGGUUGUGUAGACACAAGAAAGGGAUG | 5239 |
| Db | 4809 | TCAATTATGGGAAACGATTTCAAAGACTAGGAAGAGTCGGTAGACACAAGCCAGGTCAAG | 4868 |
| Qy | 5240 | CAAUAGAAUUGAAUAACAUAUUAAGGAUUGAUUGAGAUUCCUAGUCUUGUGCGCACAC | 5299 |
| Db | 4869 | CTTTACGAATTTGGCCACAGAAAAGGTTTAGCGAGGTCCCAGTTGTCATAGCAACGG | 4928 |
| Qy | 5300 | AGGCUGCAUUAUUGCUCAUAUUGGAUUGCCUGUAUGACAACAAGGAGUUUCAGUUA | 5359 |
| Db | 4929 | AAAGTGTCTTAAAGTGTCTCACTTACGACTTCCAGTATATCAACAATGTTTCAACAA | 4988 |
| Qy | 5360 | ACAGUUUAUCAAUUGCAGACUCCGACGACGAGUUUAUGUCUGUUUUGAGUUGCGCG | 5419 |
| Db | 4989 | GCATTCCTGTTAATGTACGCGTAAAGCAGGACGCAACCATGTCAAGTTCGAGATCACAC | 5048 |
| Qy | 5420 | CUUACUUUUGGCUUACUUGUAUUAUUGAUGGCGACGCAUCCUGAUAUUAUUAUUAUUA | 5479 |
| Db | 5049 | CATTTTACACAAGCCAGGTGGTTAGATATACCGGATCGATTCGCAAGTACATGCAC | 5108 |
| Qy | 5480 | AUUUAUUCUUACAAGUAUAGAAUUCUGAAAUUCAAUUAGUGCCCAUGCCGUUUUAACU | 5539 |
| Db | 5109 | TCCTACAGAGATTCAGCTCAGGATTTCTGAGATAGTCTTAATAGTTAGTCCATACCCA | 5168 |
| Qy | 5540 | UUAACCGUAACAUAUUUGGCUAGUUGUAAAUUUUUAUGACAGUAUAGGAUUAUUAUUA | 5599 |
| Db | 5169 | ATCGAGGAATCAACGCTTGGCTTACAGCTAGCGAATATGCGCGCTTGGTCGCAATGTCG | 5228 |
| Qy | 5600 | AUUUACCGCGCAAGCAAAAUUCCAUUUGUAAGAAUUAUCCCAAGUAUUGAAUUAUUAU | 5659 |
| Db | 5229 | AGGATAGCGCTGATGTGAGGATTCCTTTTCATGTGCGTGAATATCCAGAGAAACTCCACC | 5288 |
| Qy | 5660 | GACAUUUGGGAAGUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU | 5719 |
| Db | 5289 | TGGAGATGTGGGATGTAGTTTCAAGGTTCAAGGTTGATGCAAGGTTTGGGCGCTCTTCTA | 5348 |
| Qy | 5720 | UUGUAGCGCAACAAGUAGCAUAUACAUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU | 5779 |
| Db | 5349 | CGCTACGCGCAAGCAAGTGGCATAACATTAACAACAGACGCTCAACTCTCATTCACGAA | 5408 |
| Qy | 5780 | CUUUGGAUAUUAUUGACCGCCUUGCAAGAAUUAUUAUUAUUAUUAUUAUUAUUAUUAU | 5839 |
| Db | 5409 | CAGTCACTATTATCGATATACATTAATTTCTGAAAGAGGAAAGACAGGATATCTTCAAAA | 5468 |
| Qy | 5840 | CAUACAAGUAACGCAUUAUGGGAACACUUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU | 5899 |
| Db | 5469 | CAGTAACGTCTAATTTGTTGTTCTTCTTCAAGTTCTCACTACAGAGCATCACAAATGCAA | 5528 |
| Qy | 5900 | UACGGAAACCAUAUUGCAAGGACUACUCUGCGCAUAUUAUUAUUAUUAUUAUUAUUAUUA | 5959 |

| | |
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| JOURNAL REFERENCE | potato A. potyvirus |
| AUTHORS | Phytopathology 88, 311-321 (1998) |
| TITLE | Kekarainen, T., Merits, A., Orueta-Barria, I., Rajamaeki, M. and Valkonen, J. P. T. |
| JOURNAL REFERENCE | Comparison of the complete sequences of five different isolates of potato A. potyvirus (PVA) |
| AUTHORS | Arch. Virol. 144, 1-12 (1999) |
| TITLE | 3 (bases 1 to 9587) |
| JOURNAL REFERENCE | Kekarainen, T. |
| AUTHORS | Direct Submission |
| TITLE | Submitted (16-DEC-1998) Kekarainen T., Dept. Plant Biology, Swedish University of Agricultural Sciences (SLU), P.O. Box 7080, Uppsala, S-75007, SWEDEN |
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| Qy | 2383 | AGCCAAUACAAGAGUUCGAGUUGGUAUAUUAUGUAACAAGAAAAGAGAGUUGUUAC | 2442 |
| Db | 1857 | GAGTCGATCGAGAAGAGGCTGTACAAAGGCTTGTGTAGCATGACGATAACAATTAT | 1916 |
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| Db | 1977 | ATGCCAACCAAGAACCACTTGTAAATTGGGTAACTCAGCTGACCCAAAGTTCTTAGACTTG | 2036 |
| Qy | 2563 | C---CAAGACGCUACAGUACAUGAUUGUGGCUAAGGAAGGUUAUGUUAUCUACAUAU | 2619 |
| Db | 2037 | CCCACAGACATTAGCACACAAATGTACATAGCCAAATCAGGATACTGTTACATAAATATA | 2096 |
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| Qy | 2680 | AGAGUAUAUUGUACCGCGUCUGCAUUGGCCAAGCUUUAUCGAUUGUCAAACUGAA | 2739 |
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| Db | 2277 | GTTGTCACGATCTCAAAACAATGCACGTGATTGTTCTTAGCTCCTCACTCAACAGGA | 2336 |
| Qy | 2860 | UUUCAUGUUCUGAAGGCAAAUAUCUGUAAGUCAGCAUUAUUAUUGCCGAUUAAGCUUG | 2919 |
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| Db | 2397 | GACTCTGAATGAACACTACAGGTTTGGAGGCACTCCAAATTCTCAGATCAATGGATAC | 2456 |
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| Db | 2994 | ATTGTTGTCAAGCCAGAAAGCGCAGTAGACTTAGGAGGAATCTACGCTACATCTATCAG | 30533 |
| Qy | 3580 | CAGUUUAUAUCAUGUAUGAAACCUUGUCAAGAAUUCUUGUAUAAAGCAAGAGUAUCU | 36339 |
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| Qy | 3880 | AUAAAGAUCAAUCCAGACCUGACAAAGGAAGAAUUAUAAAGGAGUACUAUGCAAGAAGUAGA | 39399 |
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| Db | 3654 | GAGAAGAACATGACCATCTCGATTTTCGATCTCGGACACAGACACAATCTGTCGCAAGAGCAT | 37133 |
| Qy | 4240 | AAGGAGUAGAAUUTUUGCCGCAUGGUGGAAAAAACAACUAAUUGUAUAGAGUGGUACCC | 42999 |

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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|----|-------|-----|------|---|-----------|---------------------|
| 21 | 495 | 4.9 | 1739 | 2 | AAQ54488 | Aaq54488 Potyvirus |
| 22 | 456.8 | 4.5 | 1974 | 2 | AAQ80212 | Aaq80212 Potyvirus |
| 23 | 456.8 | 4.5 | 1974 | 2 | AAQ79006 | Aaq79006 Potyvirus |
| 24 | 443.8 | 4.4 | 2005 | 2 | AAQ77849 | Aax77849 Ribozyme |
| 25 | 414.4 | 4.1 | 1107 | 2 | AAQ82836 | Aaq82836 Large rep |
| 26 | 351 | 3.5 | 1488 | 2 | AAQ97624 | Aaq97624 Nuclear i |
| 27 | 346 | 3.4 | 1479 | 2 | AAQ99252 | Aax99252 Potyvirus |
| 28 | 338.2 | 3.3 | 864 | 8 | ABT114046 | Abt114046 Papaya ri |
| 29 | 338.2 | 3.3 | 864 | 8 | AAQ49841 | Aad49841 Papaya ri |
| 30 | 329.6 | 3.2 | 864 | 8 | ABT114045 | Abt114045 Papaya ri |
| 31 | 329.6 | 3.2 | 864 | 8 | AAQ49840 | Aad49840 Papaya ri |
| 32 | 328.6 | 3.2 | 864 | 8 | ABT114049 | Abt114049 Papaya ri |
| 33 | 328.6 | 3.2 | 864 | 8 | AAQ49844 | Aad49844 Papaya ri |
| 34 | 326.8 | 3.2 | 921 | 8 | ABT114044 | Abt114044 Papaya ri |
| 35 | 326.8 | 3.2 | 921 | 8 | AAQ49839 | Aad49839 Papaya ri |
| 36 | 326 | 3.2 | 861 | 8 | ABT114043 | Abt114043 Papaya ri |
| 37 | 326 | 3.2 | 861 | 8 | AAQ49838 | Aad49838 Papaya ri |
| 38 | 325.8 | 3.2 | 792 | 2 | AAQ55667 | Aaq55667 Antisense |
| 39 | 325.8 | 3.2 | 792 | 2 | AAQ55665 | Aaq55665 TEV CP ge |
| 40 | 325.8 | 3.2 | 792 | 2 | AAQ558586 | Aat558586 Antisense |
| 41 | 325.8 | 3.2 | 792 | 2 | AAQ558584 | Aat558584 Modified |
| 42 | 325.8 | 3.2 | 793 | 2 | AAQ55666 | Aaq55666 Truncated |
| 43 | 325.8 | 3.2 | 793 | 2 | AAQ558585 | Aat558585 Modified |
| 44 | 325.4 | 3.2 | 1797 | 2 | AAT34661 | Aat34661 Nta prote |
| 45 | 324.8 | 3.2 | 864 | 8 | ABT114042 | Abt114042 Papaya ri |

ALIGNMENTS

| | |
|----------|---|
| RESULT 1 | |
| ABQ83443 | |
| ID | ABQ83443 standard; RNA; 10155 BP. |
| XX | |
| AC | ABQ83443; |
| XX | |
| DT | 21-JAN-2003 (first entry) |
| XX | |
| DE | Papaya leaf-distortion mosaic virus genomic RNA SEQ ID NO:1. |
| XX | |
| KW | Papaya leaf-distortion mosaic virus; PLDMV; infection; resistance; gene; ss. |
| XX | |
| OS | Papaya leaf-distortion mosaic potyvirus. |
| XX | |
| FH | Key Location/Qualifiers |
| FT | CDS 136..9945 |
| FT | /*tag= a |
| FT | /product= "Papaya leaf-distortion mosaic virus protein" |
| XX | |
| PN | JP2002238574-A. |
| XX | |
| PD | 27-AUG-2002. |
| XX | |
| PF | 16-FEB-2001; 2001JP-00040523. |
| XX | |
| PR | 16-FEB-2001; 2001JP-00040523. |
| XX | |
| PA | (DOKU-) DOKURITSU GYOSEI HOJIN KOKUSAI NORINSUIS. |
| XX | |
| DR | WPI; 2003-003951/01. |
| DR | P-PSDB; ABP54436. |
| XX | |
| PT | A full length genomic RNA of papaya leaf-malformation mosaic virus, useful for creating a papaya leaf-malformation mosaic virus-resistant plant, comprises a sequence where a uracil is replaced by a thymine. |
| XX | |
| PS | Claim 1; Page 7-20; 31pp; Japanese. |
| XX | |
| CC | The present sequence represents the full length genomic RNA (S1) of papaya leaf-distortion mosaic virus (papaya leaf-distortion mosaic potyvirus) which is useful for creating a papaya leaf-distortion mosaic virus-resistant plant. The RNA sequence comprises a sequence where a |

Db 1922 CGCAAAACAAUUGCACAAAUUATUGGACGUCGCCAAAGAGAUUCCUUUUUCAAUUUAG 1981
Qy 1982 AGCAUCUGAUAUGAAUUGCUAAUUAAGUCGGAUAAACUUGUUAGCGAGGAUUCUUAUGAAA 2041
Db 1982 AGCAUCUGAUAUGAAUUGCUAAUUAAGUCGGAUAAACUUGUUAGCGAGGAUUCUUAUGAAA 2041
Qy 2042 UGUUCUAAGCCUUUUAAGACUACACGCTUGGCAUAAAAAACAGGAGCGAUUCUUAUGA 2101
Db 2042 UGUUCUAAGCCUUUUAAGACUACACGCTUGGCAUAAAAAACAGGAGCGAUUCUUAUGA 2101
Qy 2102 AGGAGAGAUUCACCAUUCUGGAAUAAGAUGUCAGGUAAAGCACAAUUAUUAUUGCAU 2161
Db 2102 AGGAGAGAUUCACCAUUCUGGAAUAAGAUGUCAGGUAAAGCACAAUUAUUAUUGCAU 2161
Qy 2162 UGAUGUGUGACAACCAACUUGACAACAAAUUGGUAACUUCUGUGGGGUGAAAGAGUUUUC 2221
Db 2162 UGAUGUGUGACAACCAACUUGACAACAAAUUGGUAACUUCUGUGGGGUGAAAGAGUUUUC 2221
Qy 2222 AUGCGAAGAGUUUUUCUUAACUUCUUUGAGAAAGUUGAUUCACUAGCGGUUAUAGA 2281
Db 2222 AUGCGAAGAGUUUUUCUUAACUUCUUUGAGAAAGUUGAUUCACUAGCGGUUAUAGA 2281
Qy 2282 AACACAUUAUUGCGAGUACCAACUUGGCAAGACAAACAGCUUAUAGGAAACUCGANUTU 2341
Db 2282 AACACAUUAUUGCGAGUACCAACUUGGCAAGACAAACAGCUUAUAGGAAACUCGANUTU 2341
Qy 2342 UAUCGACGGAUCCAUUCUACGCUACGACAAACAAUUGAAGGUAAGCCCAUACACAGAGUUC 2401
Db 2342 UAUCGACGGAUCCAUUCUACGCUACGACAAACAAUUGAAGGUAAGCCCAUACACAGAGUUC 2401
Qy 2402 CAGUUGUAAAUUUGUAACAGCAAAAGAGAUUGGUUUAUGUUAUCUACGUAUCUACGAGUUG 2461
Db 2402 CAGUUGUAAAUUUGUAACAGCAAAAGAGAUUGGUUUAUGUUAUCUACGUAUCUACGAGUUG 2461
Qy 2462 UUAACAUGGAAGUUGUACGCCAUUGUUAUUGUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 2521
Db 2462 UUAACAUGGAAGUUGUACGCCAUUGUUAUUGUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 2521
Qy 2522 UAGUCAUUGGAAAUUCACGAGAGAUCCAAAGAUUGUGAUGUACCAAGCAGCUCAAGUGACA 2581
Db 2522 UAGUCAUUGGAAAUUCACGAGAGAUCCAAAGAUUGUGAUGUACCAAGCAGCUCAAGUGACA 2581
Qy 2582 UGAUUGUGGUCAAGGAAGGUUAUUGUUAUCUUAACAUUUUUCUUGGCAUUGUUGCUGAUG 2641
Db 2582 UGAUUGUGGUCAAGGAAGGUUAUUGUUAUCUUAACAUUUUUCUUGGCAUUGUUGCUGAUG 2641
Qy 2642 UGAUUGAGAGUGAAUCAAUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 2701
Db 2642 UGAUUGAGAGUGAAUCAAUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 2701
Qy 2702 UCGGUCAAUUGGCCAAAGCUAAUUGGUGUUGCAACUGAAUUGUUAUUCUUAUACAGCCUUC 2761
Db 2702 UCGGUCAAUUGGCCAAAGCUAAUUGGUGUUGCAACUGAAUUGUUAUUCUUAUACAGCCUUC 2761
Qy 2762 ACCUCGAAACGAAAUUUGCUGAGUGGCCGCAAUUCUAGUGGAUCAUAUUAUUAUUAUUA 2821
Db 2762 ACCUCGAAACGAAAUUUGCUGAGUGGCCGCAAUUCUAGUGGAUCAUAUUAUUAUUAUUA 2821
Qy 2822 UGCAUGAGUAGUUAUUAUUGGCUUGAGACGCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 2881
Db 2822 UGCAUGAGUAGUUAUUAUUGGCUUGAGACGCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 2881
Qy 2882 CUGUAAAGUCAGUAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 2941
Db 2882 CUGUAAAGUCAGUAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 2941
Qy 2942 UAGUAGUGGAGACUUCUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3001
Db 2942 UAGUAGUGGAGACUUCUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3001
Qy 3002 AAUGUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3061
Db 3002 AAUGUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3061

Qy 3062 UUUUAGCGUGUAUUCUACCAAGGUGUUUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3121
Db 3062 UUUUAGCGUGUAUUCUACCAAGGUGUUUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3121
Qy 3122 UAGCUUUAAGUACUUGGAGUGACGACACAGUCUGUCGUCGUCUUAUUAUUAUUAUUAUUA 3181
Db 3122 UAGCUUUAAGUACUUGGAGUGACGACACAGUCUGUCGUCGUCUUAUUAUUAUUAUUAUUA 3181
Qy 3182 AUGGACUAGCUGCAAAAGUAAACAGUUGUCUAAACAUUUAUUAUUAUUAUUAUUAUUAUUA 3241
Db 3182 AUGGACUAGCUGCAAAAGUAAACAGUUGUCUAAACAUUUAUUAUUAUUAUUAUUAUUAUUA 3241
Qy 3242 AACCGGGGCGCGCAAAUUTUGAUUUCGUGCAUGGAAACCAUACAUUGAACAAGCCAUUCAU 3301
Db 3242 AACCGGGGCGCGCAAAUUTUGAUUUCGUGCAUGGAAACCAUACAUUGAACAAGCCAUUCAU 3301
Qy 3302 ACCAACCCCGCGUCUUCUUAACUACAGGUCAGGCAAAUCGUAAGACAUUAUUAUUAUUAUUA 3361
Db 3302 ACCAACCCCGCGUCUUCUUAACUACAGGUCAGGCAAAUCGUAAGACAUUAUUAUUAUUAUUA 3361
Qy 3362 UUGAUCUCUCCCGGATUCAGCAUUAUCAAUCUGAAGAUAGUAUUGUAUUGAUGGAAUUA 3421
Db 3362 UUGAUCUCUCCCGGATUCAGCAUUAUCAAUCUGAAGAUAGUAUUGUAUUGAUGGAAUUA 3421
Qy 3422 GUUAUCUCUUGGAAUUAUAGAGAUUCGUGGAAACGACUUAUUAAGUGGUGGAAUUAUUA 3481
Db 3422 GUUAUCUCUUGGAAUUAUAGAGAUUCGUGGAAACGACUUAUUAAGUGGUGGAAUUAUUA 3481
Qy 3482 AAUUGGCGAUUUAUUAAGUAUCUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3541
Db 3482 AAUUGGCGAUUUAUUAAGUAUCUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3541
Qy 3542 CUACCGAUUUAUGCGGUGCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3601
Db 3542 CUACCGAUUUAUGCGGUGCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3601
Qy 3602 AACCTGUCUAGAAAUUCUUGUGUAAAGCAAGAGAUACUUGUAAGGAUUAUUAUUAUUA 3661
Db 3602 AACCTGUCUAGAAAUUCUUGUGUAAAGCAAGAGAUACUUGUAAGGAUUAUUAUUAUUAUUA 3661
Qy 3662 CAAACUCCUGGACAUUUCGGGCAACAUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3721
Db 3662 CAAACUCCUGGACAUUUCGGGCAACAUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3721
Qy 3722 UGAAGUUUAUAAACAUUCUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3781
Db 3722 UGAAGUUUAUAAACAUUCUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3781
Qy 3782 AUUCUUAUUAUUCGACUUAUGCAACAAUUGAAGAGAGAAAGCAGGUGAAUUAUUAUUAUUA 3841
Db 3782 AUUCUUAUUAUUCGACUUAUGCAACAAUUGAAGAGAGAAAGCAGGUGAAUUAUUAUUAUUA 3841
Qy 3842 UUCUGAUGAAUUAUUAUUGGCGCUUUAUUAAGGACGAGAAUUAAGAUCAUUAUUAUUAUUA 3901
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Qy 3902 CAAAGGAGAAUUAUUAAGGAGUAUUAUUGCAAGAGUAGACUUGAGGUGAUUUAUUAUUAUUA 3961
Db 3902 CAAAGGAGAAUUAUUAAGGAGUAUUAUUGCAAGAGUAGACUUGAGGUGAUUUAUUAUUAUUA 3961
Qy 3962 AUAAAGAAUUAUUAAGAAAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 4021
Db 3962 AUAAAGAAUUAUUAAGAAAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 4021
Qy 4022 AGAAAUUAUUAUUAUUAUUGGCUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 4081
Db 4022 AGAAAUUAUUAUUAUUAUUGGCUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 4081
Qy 4082 GUGUAUUAUUAAGACACUGAAACAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 4141
Db 4082 GUGUAUUAUUAAGACACUGAAACAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 4141

| | | | | | |
|----|------|----------------------------|-----------------------------|--------------|------|
| QY | 4142 | CA CAUCAAAGCUTUGAGCAGCAUUC | CAAGACAUCUUGACUCACAAAGAAACA | CAUUGAUU | 4201 |
| Db | 4142 | CA CAUCAAAGCUTUGAGCAGCAUUC | CAAGACAUCUUGACUCACAAAGAAACA | CAUUGAUU | 4201 |
| QY | 4202 | UCGACUUAUGUUGAGGGGAGCAAA | AGUUAACAGAUUCAAGGAGAUAA | CUUUGCGCAU | 4261 |
| Db | 4202 | UCGACUUAUGUUGAGGGGAGCAAA | AGUUAACAGAUUCAAGGAGAUAA | CUUUGCGCAU | 4261 |
| QY | 4262 | GGUGGAAAAAACAUAUAUUGUA | UAGAGUGGUACCCAUUAUAGAAC | CAACUGGGAAAU | 4321 |
| Db | 4262 | GGUGGAAAAAACAUAUAUUGUA | UAGAGUGGUACCCAUUAUAGAAC | CAACUGGGAAAU | 4321 |
| QY | 4322 | UUAUUGAAUUCACUCUGUGAAAG | CGUGUUAUGUGAGUAACAACAUAU | CUCAUGCCCUG | 4381 |
| Db | 4322 | UUAUUGAAUUCACUCUGUGAAAG | CGUGUUAUGUGAGUAACAACAUAU | CUCAUGCCCUG | 4381 |
| QY | 4382 | AGAAAGAAUUGGAUAGUCGUGG | UGUGUAGUAACAGGAAAUUCACUG | GUACCAUUGC | 4441 |
| Db | 4382 | AGAAAGAAUUGGAUAGUCGUGG | UGUGUAGUAACAGGAAAUUCACUG | GUACCAUUGC | 4441 |
| QY | 4442 | CGUUAUCUAUAAAGCGCAGUUCU | UAUGCUGAACCAACAAGCAUUGG | CAGAGAAUG | 4501 |
| Db | 4442 | CGUUAUCUAUAAAGCGCAGUUCU | UAUGCUGAACCAACAAGCAUUGG | CAGAGAAUG | 4501 |
| QY | 4502 | UCUCACGACAGUUGAGACAACAUC | CUUUAUGCAAACCCCAUUGAGAAU | UGCGAGGAA | 4561 |
| Db | 4502 | UCUCACGACAGUUGAGACAACAUC | CUUUAUGCAAACCCCAUUGAGAAU | UGCGAGGAA | 4561 |
| QY | 4562 | UGUCAUCUUVUGGAUCUAGUAAU | AUAUGUAUAUGACUAGUGAUUUG | CUUUAUUAU | 4621 |
| Db | 4562 | UGUCAUCUUVUGGAUCUAGUAAU | AUAUGUAUAUGACUAGUGAUUUG | CUUUAUUAU | 4621 |
| QY | 4622 | UUGCAAUAUUCUUAUUAUUAUG | AUUAUGAUUUGAAUUAUGAGUGU | CACG | 4681 |
| Db | 4622 | UUGCAAUAUUCUUAUUAUUAUG | AUUAUGAUUUGAAUUAUGAGUGU | CACG | 4681 |
| QY | 4682 | UCCUAGAUAGCAACGUAUUGGCAU | UCUGUUCUUAAGAAACAACUAUGG | CA | 4741 |
| Db | 4682 | UCCUAGAUAGCAACGUAUUGGCAU | UCUGUUCUUAAGAAACAACUAUGG | CA | 4741 |
| QY | 4742 | AAACUUAUGAAUGUCAGCCACCA | CCACAGGGCGGUGAAUUGAAUUC | CAACACAGCAUC | 4801 |
| Db | 4742 | AAACUUAUGAAUGUCAGCCACCA | CCACAGGGCGGUGAAUUGAAUUC | CAACACAGCAUC | 4801 |
| QY | 4802 | CAGUUCUUAUUAUAGGAACAACU | TAGUUAUUGCAAGCUUUAUGAGU | CAAGAA | 4861 |
| Db | 4802 | CAGUUCUUAUUAUAGGAACAACU | TAGUUAUUGCAAGCUUUAUGAGU | CAAGAA | 4861 |
| QY | 4862 | CUGGGUUCGACGAGAGUAUACUAU | AGGGAGACAACAUUUAUGUUAUGU | UUGUUAU | 4921 |
| Db | 4862 | CUGGGUUCGACGAGAGUAUACUAU | AGGGAGACAACAUUUAUGUUAUGU | UUGUUAU | 4921 |
| QY | 4922 | ACAAUGAGGUGAUCAGUCUCUCAA | AAAUUGCUGGAGUAUAGGCUUAU | UAGUACUAAAG | 4981 |
| Db | 4922 | ACAAUGAGGUGAUCAGUCUCUCAA | AAAUUGCUGGAGUAUAGGCUUAU | UAGUACUAAAG | 4981 |
| QY | 4982 | UCGAUGGGGCUACCAUGAAAUUG | GUUCGACCAUUAAGGAGUAGCCAG | A | 5041 |
| Db | 4982 | UCGAUGGGGCUACCAUGAAAUUG | GUUCGACCAUUAAGGAGUAGCCAG | A | 5041 |
| QY | 5042 | AGAAACAUTUUAUUGUAGCAACA | CAUAUUGGAGAAUGGAGUAGUAGU | A | 5101 |
| Db | 5042 | AGAAACAUTUUAUUGUAGCAACA | CAUAUUGGAGAAUGGAGUAGUAGU | A | 5101 |
| QY | 5102 | UUGUUGGACUUVUGUUAUAGUA | CAUCUGCUGAAAUUGAUACGACAA | CCGGUGGUUA | 5161 |
| Db | 5102 | UUGUUGGACUUVUGUUAUAGUA | CAUCUGCUGAAAUUGAUACGACAA | CCGGUGGUUA | 5161 |
| QY | 5162 | AUUAACAAGACCAUUAUUAUUAU | CGGAGAACCAUAAGAUUUGGCGU | UGUUA | 5221 |
| Db | 5162 | AUUAACAAGACCAUUAUUAUUAU | CGGAGAACCAUAAGAUUUGGCGU | UGUUA | 5221 |
| QY | 5222 | GACACAAGAAAGGCAUGCAUUGA | AAUUGGAACUAACAAUUAAGGAU | UGAUGAUUC | 5281 |

| | | | | | |
|----|------|--------------------------|-------------------------|-----------------------|------|
| Db | 5222 | GACACAAGAAAGGCAUCCAAUGAG | AUUGGAACUAACAUAUAGGAUUG | AUGAGAUUC | 5281 |
| QY | 5282 | CUAGUCUUGUGCGCAGACAGCGC | UGCAUUAUUGGCUUACAUUUGG | AUUGGCUUUAUGA | 5341 |
| Db | 5282 | CUAGUCUUGUGCGCAGACAGCGC | UGCAUUAUUGGCUUACAUUUGG | AUUGGCUUUAUGA | 5341 |
| QY | 5342 | CACAAGGAGUUCAGUUAACAAGU | UAUUAUUGCAGAGCCGACAGGCU | UUAUGU | 5401 |
| Db | 5342 | CACAAGGAGUUCAGUUAACAAGU | UAUUAUUGCAGAGCCGACAGGCU | UUAUGU | 5401 |
| QY | 5402 | CUCGUUUUAGTUGCGCGCUUACU | UAUUGGCUUACAUUUGGCUUUAU | UUGGCUUUAUGA | 5461 |
| Db | 5402 | CUCGUUUUAGTUGCGCGCUUACU | UAUUGGCUUACAUUUGGCUUUAU | UUGGCUUUAUGA | 5461 |
| QY | 5462 | ACCCUGAAAUUACAAGCAUUAU | UUAUCCUUAACAAGUUAUUGCU | UAUUAUUGGCUUUAUGA | 5521 |
| Db | 5462 | ACCCUGAAAUUACAAGCAUUAU | UUAUCCUUAACAAGUUAUUGCU | UAUUAUUGGCUUUAUGA | 5521 |
| QY | 5522 | GUGCCAUUGGCUUUAACAACUUA | CCGUUAACUUAUUGGCUUUAUUG | CUAUAUUGA | 5581 |
| Db | 5522 | GUGCCAUUGGCUUUAACAACUUA | CCGUUAACUUAUUGGCUUUAUUG | CUAUAUUGA | 5581 |
| QY | 5582 | GUUAAGGAUUCUUAUUGGCUU | UAUCCGCGCGAAGCAAAAUUCC | AUUAUUGGCUUUAUGA | 5641 |
| Db | 5582 | GUUAAGGAUUCUUAUUGGCUU | UAUCCGCGCGAAGCAAAAUUCC | AUUAUUGGCUUUAUGA | 5641 |
| QY | 5642 | UCCGAGUAUAGAAUACCGACA | CUUUGGCGAAGUUAUUAUUAU | UUAUUGGCUUUAUGA | 5701 |
| Db | 5642 | UCCGAGUAUAGAAUACCGACA | CUUUGGCGAAGUUAUUAUUAU | UUAUUGGCUUUAUGA | 5701 |
| QY | 5702 | GUUUUGGUAAGUAGUGUUGUUA | AGCGCAACAAAGUAGCAUUAACA | CUUUAUUAUUGA | 5761 |
| Db | 5702 | GUUUUGGUAAGUAGUGUUGUUA | AGCGCAACAAAGUAGCAUUAACA | CUUUAUUAUUGA | 5761 |
| QY | 5762 | UUAUUAUUGGAAAUUUAUUGA | CGCCCUUUGCAAGAAAUUAUAG | A | 5821 |
| Db | 5762 | UUAUUAUUGGAAAUUUAUUGA | CGCCCUUUGCAAGAAAUUAUAG | A | 5821 |
| QY | 5822 | AAACAGCAUUAUUAAGCAUUA | AGCAUUAAGCAUUAUUAUUAU | UUAUUGGCUUUAUGA | 5881 |
| Db | 5822 | AAACAGCAUUAUUAAGCAUUA | AGCAUUAAGCAUUAUUAUUAU | UUAUUGGCUUUAUGA | 5881 |
| QY | 5882 | UAAGCAUUAAGCAUUAAGCAU | UAAGCAUUAAGCAUUAAGCAU | UAAGCAUUAAGCAUUAAGCAU | 5941 |
| Db | 5882 | UAAGCAUUAAGCAUUAAGCAU | UAAGCAUUAAGCAUUAAGCAU | UAAGCAUUAAGCAUUAAGCAU | 5941 |
| QY | 5942 | AGAAAUUGCAGCAGCAAGAAU | CAAAUUAUGGAAUUAUUAUUAU | UUAUUAUUAUUAUUAUUAU | 6001 |
| Db | 5942 | AGAAAUUGCAGCAGCAAGAAU | CAAAUUAUGGAAUUAUUAUUAU | UUAUUAUUAUUAUUAUUAU | 6001 |
| QY | 6002 | CGGCGAAAUUGCGGAUUC | CAAGAUUUGGAGUUAUUAUUAU | UUAUUAUUAUUAUUAUUAU | 6061 |
| Db | 6002 | CGGCGAAAUUGCGGAUUC | CAAGAUUUGGAGUUAUUAUUAU | UUAUUAUUAUUAUUAUUAU | 6061 |
| QY | 6062 | AGAAAUUAUUAUUAUUAUUAU | UUAUUAUUAUUAUUAUUAUUAU | UUAUUAUUAUUAUUAUUAU | 6121 |
| Db | 6062 | AGAAAUUAUUAUUAUUAUUAU | UUAUUAUUAUUAUUAUUAUUAU | UUAUUAUUAUUAUUAUUAU | 6121 |
| QY | 6122 | AUAUUAUUAUUAUUAUUAUUAU | UUAUUAUUAUUAUUAUUAUUAU | UUAUUAUUAUUAUUAUUAU | 6181 |
| Db | 6122 | AUAUUAUUAUUAUUAUUAUUAU | UUAUUAUUAUUAUUAUUAUUAU | UUAUUAUUAUUAUUAUUAU | 6181 |
| QY | 6182 | AAUUAUAUUAUUAUUAUUAUUAU | UUAUUAUUAUUAUUAUUAUUAU | UUAUUAUUAUUAUUAUUAU | 6241 |
| Db | 6182 | AAUUAUAUUAUUAUUAUUAUUAU | UUAUUAUUAUUAUUAUUAUUAU | UUAUUAUUAUUAUUAUUAU | 6241 |
| QY | 6242 | GGGAUUGCGCAUUAUUAUUAUUAU | UUAUUAUUAUUAUUAUUAUUAU | UUAUUAUUAUUAUUAUUAU | 6301 |
| Db | 6242 | GGGAUUGCGCAUUAUUAUUAUUAU | UUAUUAUUAUUAUUAUUAUUAU | UUAUUAUUAUUAUUAUUAU | 6301 |
| QY | 6302 | AUUAUUAUUAUUAUUAUUAUUAU | UUAUUAUUAUUAUUAUUAUUAU | UUAUUAUUAUUAUUAUUAU | 6361 |

Weakly toxic strain of *Dioscoreaceae* mosaic virus used in the genetic diagnosis of the mosaic virus infection and for the management of crops resistant to the virus.

Claim 1; Page 6-20; 22pp; Japanese.

The present sequence encodes the Japanese yam mosaic virus (JYMV) JYMV-M protein sequence. JYMV is a weakly toxic strain of Dioscoreaceae mosaic virus. The present invention also describes: (1) a weakly toxic strain of Dioscoreaceae mosaic virus having a nucleic acid sequence which shows interference against the infection of a strongly toxic strain of Dioscoreaceae mosaic virus; (2) a Dioscoreaceae mosaic virus-resistant crop which is a plant of *Dioscorea japonica*, *Dioscorea opposita* or *Dioscorea alata* and is infected artificially by a weakly toxic strain of Dioscoreaceae mosaic virus; (3) a method for the cultivation of a Dioscoreaceae mosaic virus-resistant crop in which the weakly toxic strain of Dioscoreaceae mosaic virus is infected to the tubercle or the bulb of a plant of *Dioscorea japonica*, *Dioscorea opposita* or *Dioscorea alata* and the tubercle or bulb is grown; and (4) a method for genetic diagnosis of a Dioscoreaceae mosaic virus in which a DNA fragment amplified by using reverse transcriptase-polymerase chain reaction (RT-PCR) primers atagcttaccaccccctac (AAP28999) and caccctacatcgwagragy (AAP32201) is treated with a restriction enzyme to distinguish the weakly toxic strain of Dioscoreaceae mosaic virus from the strongly toxic strain of Dioscoreaceae mosaic virus.

Sequence 9760 BP: 3339 A: 1851 C: 2171 G: 2399 T: 0 U: 0 Other:

23.3%; Score 2363.6; DB 5; Length 9760; every Match

st Local Similarity 40.7%; Pred. No. 0;

Matches 3517; Conservative 1339; Mismatches 3669; Indels 121; Gaps 17;

[illegible]

I420 GGGCACAGUGGACAAUACAUAUCAAUAUGAUAAAGUUAGAGGUUUGAGUGGACGGCAUUC I479

979 GGACATAGTGGTTTGTCTTGAATAGAGAGACTTTATGTGGACACAAATCTCGTCATAT 1038

1480 GGAAGUUACAUCAUUGUUAGGGUAGCAUGGAUGGCAGAAUUAUUGACGUCUGUCAAAG 1539

1039 C G A B C A T A W T C A T C C T T C C C C A T C A C C C C A T A T A T C A T C A C C T A T T A A A

1039 GGAGGAGTATTCATCGTTCGTGGCATTACAGAGGGCAGTATATGATGCACGATATTAA 1098

1540 AUCACACACAGCGUUAUGAUCAACAUGACCCACUACAGUGAUGCAGGUUUGAGUUUUUGG 1599

1099 TTATCCCAACAATACGCAGGAAGATAGTGC GATTTGTCTGATCCAGCGTTAAATTTTGG 1158

1600 AAAGGTTTGTGATCGTTCAAATTATTTGACATTCGAGATTAGACCTTAAGCAACGGCTCAATGAGATGCC 1659

[illegible]

1159 AATGGGTTCAACAC-- --AGCTTTTCAAAAGATACAGGAAACAAGATCGTGAGCACACATGT 1215

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1660 AAGGCCACUAAACCGUAGGAGUGGCGAAUGGCAGCCAUGUAACCAACUCCUA 1719

1216 GAAACGGATCTTGAATGTTGAGGAGTGGTGAGGTGGCAGCCTATTGTGCTCTTGCTCTT 1275

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1720 UUUCCAAUGUGGAAAUAACAUGCACUCUCAAUGUGGAGAACUGCUUGAAAUGUUGUCAA 1779

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| 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 | 46 | 47 | 48 | 49 | 50 | 51 | 52 | 53 | 54 | 55 | 56 | 57 | 58 | 59 | 60 | 61 | 62 | 63 | 64 | 65 | 66 | 67 | 68 | 69 | 70 | 71 | 72 | 73 | 74 | 75 | 76 | 77 | 78 | 79 | 80 | 81 | 82 | 83 | 84 | 85 | 86 | 87 | 88 | 89 | 90 | 91 | 92 | 93 | 94 | 95 | 96 | 97 | 98 | 99 | 100 |

1276 TTTCTTG TGGGAAAATAACATGCAATGCAATGCTAGAGAGAGAAATTATATATCAGAAAGG 1335

1780 GAAGAGGAACUUGAAUCUUUCAGGCGUAAAGGAGCCAUUGGCAAGUAAAUUUAUCCAGU 1839

1336 CAAGCGACGCATGAAACATACTCAAGAAACAACAGGAAATACGTACACATCGTTCCTTCAA 1395

1940 CUPICANIANCA A XITPICCTPICA CCUICCANICANTHTCTPICA PCCANIANICACANIANCUCICACAN 1989

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1396 CGTCATCCACAATTCAAGCATGCTCTTCAGATACTAGAAAGGCAAGGCATTACAA 1455

1900 CGGAUGAACACAAACTUUCGAUGCGCACAAACAUAUJUGGAGUCGCAA 1959

1456 AGTGTGAAACAGCAATTATATAAGATTTTACAGAGATTCA TAGTCTCTCAGAAAGGAAACA 1515

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1960 GAGAUUCCUUUUUCAA AUUAGAGCAUCUGAAUUGCUAAUUAAGUCGGAUAAACUU 2019

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1516 CTTCCCTGCTTTTAGCCAGGCAATCGCATAAATGATGTCTCTAATAAAAGGAGGTAGTGCA 1575

2020 GTTATGGCAGGATTTCTTAUGAAATGTCCTCAATGGCTTTTATAGAGCTAACACCGTGGCAATAA 2079

ZUZU GUUAAGCCGAAGAUGUUUC UAAUUAAAUGGCU CCGAAGGGCUC GCAACAUUUUUU

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| Db | 1576 | ACAGCAGAGAAATTATCAGAAGCAACACGAAACTTGGCTTCAGATTGTTGGTATCTTTAA | 1635 |
| Qy | 2080 | AACAGGAGCGAUUUAUUCACAAAGGAGGAGAUUCCAUUUCGGAUUAAGAUUGUCAGGU | 2139 |
| Db | 1636 | AATCGAACAGAAAGTTCAGAGAAAGGAACTCTGNAACAATTTTGGAAACAAAATCTCTCAG | 1695 |
| Qy | 2140 | AAAGCACAUAUUUAUUUGCAUUAUGAUGUGUGACAACCAACUGACAAAAAUGUAACUUC | 2199 |
| Db | 1696 | AAAGCTCATCTGAACCCGACACTAAATGTGTGATAAACCCAGCTCGATGAAATGGAAATCTTT | 1755 |
| Qy | 2200 | GUGUGGGUGAAAGAGAGUUAUCGCGAAGAGGUUUUUAACUUCUUGAGAGAAAGU | 2259 |
| Db | 1756 | GTTTGGGGTGAAGAGAGGATATCATGCGAAACGGTCTTTAATAAATACTTTTGAGATTGTT | 1815 |
| Qy | 2260 | GAUUCACACGCGUUAUAAAGAAACAUAUAUUGCGAGUCAACCCAAAUAGGCAACAAGCAA | 2319 |
| Db | 1816 | GATCTTAGCAAGATATGCAAAATTTGAAGCAGCTATAAACCCAGGGGCCAACGCACA | 1875 |
| Qy | 2320 | ACAGCUAAGGAAAAUGAUUUUUGACGGAUCCAUUCUACGCUACGACAACAAAUGAAA | 2379 |
| Db | 1876 | ACAGCAATACCACAGGCTAATCGTGCCAAACAAATTTTGAAGATTTGAGAGAACAGATGCAA | 1935 |
| Qy | 2380 | GSUAGCCCAUCACAGAGUUCGAGUUGUUAUAUUGUACAGCAACAAAGAGUGGUU | 2439 |
| Db | 1936 | GGTGAATCAATTTGGAGAACACCCATTTGACTGTTGAGTGTACTAGTGACTGAATGGTGAT | 1995 |
| Qy | 2440 | UAGCUCUAUCAGCAGUCUGUUAUCAAUGGAAGUGUACGCGCAUUGUUUUCUGAUUC | 2499 |
| Db | 1996 | TTTCTGTTCCCTGTTGTTGTGTGACAAATGAAGCTGGGGAACCTATACTACTCAGATTG | 2055 |
| Qy | 2500 | AGAUGCACAAAGAUAUCUAGUACAUUGGAAAUUCAGGAGAUCCAAAGUAUGUGGAU | 2559 |
| Db | 2056 | CAAAATGCCAACAAAGAAATCATCTAGTTGTTGGAAATAGTGGGACTCCAAATACGTTGAC | 2115 |
| Qy | 2560 | GUACCAAGCAGCUCACAGUGA---CAUGAUUGGCGUAGGAAGGUUAUUGUUAUCUCAAC | 2616 |
| Db | 2116 | ATCCGCGCACAGAAGGCCAATCCATGTATATAGCCAAAGCTGGTTTTGCTACATGAAC | 2175 |
| Qy | 2617 | AUUUUCUUGCAUUGUUGCAUUGUAGUAGAGUGAAUCAAUAUCAAUAUUCACAAAGAAG | 2676 |
| Db | 2176 | ATCTTTCTTGCAATGCTTTGTATATGTGCGCAAGGAGNAGCTAAGGCATTTACAAAATG | 2235 |
| Qy | 2677 | GUUAGAGAUUAUUGUACCGCUCUGGUCAAUUGGCCAAAGCUUAUCGUGUUGCAACU | 2736 |
| Db | 2236 | GTGAGAGATGCTTTATAAATCAGCTGGGACATGGCCTACACTTTTGGACGTAGCAAGT | 2295 |
| Qy | 2737 | GAUUGUUAUUUCUACGCGCUUCCACCCUGAAACGNAAAAUGUGAGUUGCCCCGAUU | 2796 |
| Db | 2296 | GCAATGCTATCTGCTGAAGTGTCTTTTCCAGATGTCTACAGAGTGTCTAGTTGCCACGTATA | 2355 |
| Qy | 2797 | CUAGUGAUCAUACAUCAAAAUGUAGUGAUGAUCGAUUAUUAUUGCGUCGCUAGACACG | 2856 |
| Db | 2356 | ATGGTTGTCACAGACGAAACTATGCACTGTGCTAGACTCGTATGTTCTACTGAAACACT | 2415 |
| Qy | 2857 | CAAUUUAUUGUUGAAGGCAAAUACUGUAAGUCAGCUAAUUAUAAUUCGCGCAUUAUGAC | 2916 |
| Db | 2416 | GGTTATCACATCTCTAAAAGCGAACACAGTTTGAACAATTAATCAAAATTCACAGGTGCAGGT | 2475 |
| Qy | 2917 | UUGGAUUGGAGCUGGAAAACAUUAUUUUGUAGGUGGAGACCUCCUACUAGCAAGCAAG--- | 2971 |
| Db | 2476 | TTGAAATCAGATATGAAGCATTTATTTAGTTGGAGGGCCAACTACTTAAACAAATGAAGACATT | 2535 |
| Qy | 2972 | -----CUCCUCAGUGUUCUAUAAAAUUAUCUCUGUAUUUAUUAUUAUUAUUAU | 3012 |
| Db | 2536 | GATCCAACAGAGTACCGAACCATCTTTGGCATCTTAAGGAGACTCATAAAGGCATCTTAC | 2595 |
| Qy | 3013 | AGGCCUAAAUUGAUGAGGCAUUGCAUUGAGGAAGAGCGCUUUUUUGUUAUUUAGCGUGU | 3072 |
| Db | 2596 | AACCCACNAGTTCTATTAGATGACATCCGCATTTGATAGGTATCTGCTCTCTACGCATTG | 2655 |
| Qy | 3073 | AUCUCAACGAGGUGUUUAUUGCUUUUAUUAUUAUAGUCAGCAUUUAUAGAAUUAUUAAG | 3132 |

QY 5282 CUAGUCUUGUGGCGACACAGGCGUCGUAUUUUAUUAUGCUUUAUUAUGUAUUGCCUUGUAUUGA 5341
Db 4865 CTAGTTGTCATCGCAACGAGCGAGCGTTAGATGCTTCACATTCGAGCTGCTTTATCA 4924
QY 5342 CACAGGAGUUCAGAGUUAACAGUUAUCAAUUGCACAGUCCGACAGGCCAGAGUUAUGU 5401
Db 4925 CGAATAATGTGACACACAGAGCTCTCTCAATGCAACCGGTAAAGACACGACGAAATGG 4984
QY 5402 CUCGUUUUGAGUUGCCGCUUACUUAUUGCCUUCACUUGUAUAUUAUGAUGGCGAGCAUGC 5461
Db 4985 CACATTTTGAGTTGTCCCATTTTACAGGTATCATTTTGTGCGATATGATGGAACCATGC 5044
QY 5462 ACCUGAAUUAACAGCAUUAUUAUUCUUAUAAGUUAUGAUAUUAUUAUUAUUAUUA 5521
Db 5045 ACCGAGAGATTCTCAAAAGTTCTCAAAAGATTCTCAAAAGATTCTCAAAAGATTCTCA 5104
QY 5522 GUGCCAUUGGUUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 5581
Db 5105 ACAAGACTGCTATACCAATAGAGGAGTTAAACATGGATGACAGATGAGCGCATATCAGA 5164
QY 5582 GUUAUGAAUCCAUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 5641
Db 5165 GACTTGGAGCGAATGTTGGGCGACAGTAACGAAATTCGAATACCATTTTGTGCAAGAAG 5224
QY 5642 UCCAGAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 5701
Db 5225 TGCCCTGAACATTGCGCAACAAATATGCGGCATCATCAACGCGCAAGAGATGCTG 5284
QY 5702 GUUUUGUAAGUAGUUGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 5761
Db 5285 GTTTTGGACGGCTATCAGCGCTAGTGCTATGTAAGTTGCTTACACACTCAGACTGAGC 5344
QY 5762 UUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 5821
Db 5345 TGATGTCAATTCACGAAATACACATAATGATGCGCTAATGTTGAGGAAGACAAA 5404
QY 5822 AACAGAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 5881
Db 5405 AACAGAGTATTCAGGACGATTAACAAATTCATTTCTCGTCCAAATTTCTCTTC 5464
QY 5882 UAGCAUAGCAAAUUGCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 5941
Db 5465 AGAGTATGCTAATGCAATAGAGCTGATTTTCATCAGATCAGATCAGATCAGATCAG 5524
QY 5942 AGAAUUGCAGGCGACGAAAGAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 6001
Db 5525 GTGTGCTTGAGACGCAAGGCTCAGTTGTGCGCAATTTAAATTTAAACATTGACGCTG 5584
QY 6002 C-----GGCGAAUUGCGGAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 6037
Db 5585 CTTTTTCAGGACTTTGACAGTCAAGTGGGAGAGTTACATAAGCAATTTTGGCGCACTCG 5644
QY 6038 AACUAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 6097
Db 5645 ACCGAGTTATCATCATCAGAGAGCAATGATGAGCACTTAAATTAAGGGAAGAT 5704
QY 6098 GGAUAAGUCAUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 6157
Db 5705 GGAATAAGCCACTCATCACAGGACATATGATGATGATGATGATGATGATGATGATGAT 5764
QY 6158 UCUGGAUUAUUGGUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 6208
Db 5765 TTATGATGTTGATTAACAAATTCAAAAGTCAAAATGATGATGATGATGATGATGATGAT 5824
QY 6209 AAGGAAGAGGAGACUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 6268
Db 5825 AAGGAAGGACAGCGCTCAACGCTACGTTTATAGATGACGCTGACAGCAAACTCGGAA 5884
QY 6269 GAGAUAUUAUUGGAGACGCGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 6328
Db 5885 GAGAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5944
QY 6329 GAGGUGCAUUAUAGGCGCAAGAGAGAAUUGGCGGAAAUUAUUAUUAUUAUUAUUAUUA 6388

Db 5945 AAGGTAAAAACAAGTGTGTCGCAACAATGGTATGGGTCAAAAAACAACGGAAGTTTGTAAATA 6004
QY 6389 UGUUAUGGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 6448
Db 6005 TGTATTTCATTTGACCCAGAGATTTTTCAGCAGTGCCTTTGTAGATGCTCTCACAGGCG 6064
QY 6449 CAAAGCGUAGAGAGAGUCCUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 6508
Db 6065 CAACTCTTGATGAACAACCAATAACAGATCTACATTTAGTACAGGAGCATTTTCAACA 6124
QY 6509 UCAGAGACAAAUGUUAUGAGCAGGCGCUCAUGAUGGCAACAACAUUAUUAUUAUUA 6568
Db 6125 TTCGGAGTGAATGATAGAACTCAGGAGAACTCGAGAGCCAAACATTTGTATAGTGGAAA 6184
QY 6569 GUUAUGACCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 6628
Db 6185 GAGTTAAACGATATATACATGAACAATAGAACTGGAAAGGCACACTACAAGTTGATTGACAC 6244
QY 6629 CACAAUUCUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 6688
Db 6245 CACATAATCCGCTATTTGCTGCAACAACCAACCAATTCGAGGATTTTCCGAGAGAG 6304
QY 6689 AGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 6748
Db 6305 AGTATGAGCTAAGGCAACAACAGGACGCCCAAGCAATTTCTACTGAAGATGTTCTTAAG 6364
QY 6749 GGAUU-----GAAAGACGUUUUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 6799
Db 6365 CGAATGACTGTTAGCGAATAATGTTGCAACATGAAGCGCTTTTGCACAGAGGTTCCGCTG 6424
QY 6800 AUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 6859
Db 6425 ATTACAAACCCCTCTCCTCAATAACATCTCAAGCTATCAACCGCTTCTGAGGAGAGAG 6484
QY 6860 CCACAACUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 6919
Db 6485 ATACCATGTACCGACTTGTGATTTGGACCATCATCATCAAAACAGACACCTATTATTGAAC 6544
QY 6920 AAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 6979
Db 6545 ATAAATGTTGCTGACTGACTGACTGACTGACTGACTGACTGACTGACTGACTGACTG 6604
QY 6980 AGCAAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 7039
Db 6605 CAAAACTCCAGTTATATCCAGTTCCAAACCGAGATCTAAATTTTAAATTAGACTTTCCAAGG 6664
QY 7040 ACUUCGCCCUUUAUGCAGAGGUUAUGAUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 7099
Db 6665 ATATACCACTTTTCCACAAAACCTTCAGTTTCAGGCGCGGAGCGTAATGAAAAGATTT 6724
QY 7100 GUCUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 7159
Db 6725 GTATGTTGGCTCAAAATTTTCAAGCAAAAGCGTAAACAAACAGTATCAGAGACGAGCA 6784
QY 7160 AAACAUUCCACGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 7219
Db 6785 TTATATTGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6844
QY 7220 AUUUGGAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 7279
Db 6845 AATGTGATTTACTTTAGTCAGACGAGAGATGGCAACATAGTTGGTATTTATGATGCTTG 6904
QY 7280 UGAGUCAUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 7339
Db 6905 GGAGTTTCAATAATAACAATCAATTTTTCAGGATTTTCCAGAGAACTTTGTCAATCAGT 6964
QY 7340 AUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 7399
Db 6965 ATTTGTTGACTCCAGAAAAATCCCAATGATGATGATGATGATGATGATGATGATGAT 7024
QY 7400 UUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 7459

Db 2759 AUAUAUUUCGCAAAUAUAUUUUGACAUAUAUUGAUUCUUCAGGGGUAUGAGAGUACG 2818
QY 2288 UAAUGCGAGUCAAACCCAAUUGGCACAAGACAAACAGCUAUAAGAAACUAGAUUUUAUCGA 2347
Db 2819 UGAGGAGAGAAACCCAAUUGGCUCACGAAAGUUAAGCAAUUGGAAACUUAUAGUUUCCA 2878
QY 2348 CGGAUCCAUUACGCUACGACAAACAAUAGAAAGGUAGCCCAUACAAGAGUUCAGUUG 2407
Db 2879 CGAAUUUCUGUUUUAAGAGAGCAAAUAGAAAGGGGAAACCUUAUUCAGAAACAAACUUCG 2938
QY 2408 GUAAAUAUUGUAACAAGCAAAAGAGAGUUGUUUUAUCGUUAUUCAGCAUCGUCGUUUACAA 2467
Db 2939 ACRAACAUUGCAGAGCUUGCGUGACGGAUUUUUGUUAUCCAUGUUGUGUUAACAC 2998
QY 2468 UGGAAGAGUUGAGCCAUUUUUUUGUAUAUACAAGAUUGCAACUAAAGAAUACUUAUCUA 2527
Db 2999 UGGAUGAGGACAAACCUUAUUGAGUCAGAGUUUAAAUUACCAACAAAGAACCAUUAUGA 3058
QY 2528 UTGGAAUUCAGGAGAUCCAAAGUAUUGGUAUUGAUAUCCAAAGCAGCUCAAGUGACUAGU-- 2585
Db 3059 UUGAAACUUCAGGGAUCCAAAGUACGUCGACAUUGCCGACAGAUAAAGAAAGAGU 3118
QY 2586 -UGUGCUAAGGAAGGUUAUUGUUAUCUCAAUAUUUUUUGGCAUUGUUGCUGAAUUGA 2644
Db 3119 AUAUUGCGAAGGAUUAUUGUUAUUGUAUAUUAUUUGGCUAUGUUGGUCNAUGUCC 3178
QY 2645 AUGAGAGUAUAUAAAUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 2704
Db 3179 AUGAGGACAGAGGCAAGAGAUUUCAGAAACAAAGUGCGAGUUGUUAUUGGAGAGCUUG 3238
QY 2705 GUCAUUGGCCAAGCUUAUUGGAUUGGUAUUGAUAUUGAUAUUAUUAUUAUUAUUAUUAUUA 2764
Db 3239 GAAAGUGGCCAAACAUGUUGUAUUGAUGGACAGAGCAUGUGCAUUAUUGCAGUUUUCUAUC 3298
QY 2765 CUGAAACGAAAUUAUGAGUUGCCCGGAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 2824
Db 3299 CCGAGACGCGGAUUGCAGAACUCCCAAGAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3358
QY 2825 AUGUGAUCGAUUAUUGGCGUCGUAACACGCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 2884
Db 3359 ACGUUGAUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3418
QY 2885 UAAGUCAGCUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 2944
Db 3419 UGAGCCAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3478
QY 2945 UAAGUGGAGACCCCAUAGCAAGCAAGCUCUCAGUGUUCCAUAAAUUAUUAUUAUUAUUA 3004
Db 3479 UUGUGUGUUAUACAGCAUAUACAGAUUAUUAAGAGAGAUUGCAUACAGCAUUAUUAUUA 3538
QY 3005 GUUAUAUAUAGGCUAAAUUAUAGAGCAAUUGCAUUGAGGAAGCCUUUUUUGUUAUUA 3064
Db 3539 GAGUGUAACAAACAGACGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3598
QY 3065 UAAGUGUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3124
Db 3599 UAAGUGUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3658
QY 3125 CUUUAAGUAUUGGAGUAGCAAGCAACAGUCUGUCGUCUUUAUUAUUAUUAUUAUUAUUA 3184
Db 3659 CAUUGAGCAUUGGAUUAUACAGAGAUACAGGAAGUUGCUGUGUAUUAUUAUUAUUAUUA 3718
QY 3185 GAUAGUCGCAAAAGUAACAGUUGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3244
Db 3719 AGCUUGCAAAAGAGUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3778
QY 3245 GCGGGCGCGCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3304
Db 3779 GUCAAGCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3838
QY 3305 AACCAGCGCUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3364

Db 3839 CACUUUUCACAGAGAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3898
QY 3365 AUCUGCCGGAUUCAGCAUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3424
Db 3899 AUGAAACAAGGGCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3958
QY 3425 AUCUCAUGGAUUUACAGAGAUUUCUGGAAACGACUUAUUAUUAUUAUUAUUAUUAUUA 3484
Db 3959 GGAUUGUUCUUUUUAAAGAGAGGAUAUACGAAGGCGCCGUGGCAUGGAUUAUUAUUA 4018
QY 3485 UGUGCGAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3544
Db 4019 UCAUGGGAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 4078
QY 3545 CCGAUUUAAGCGGUGAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3604
Db 4079 GCGCUUUAAGCGAGAGAGAAACAGACUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 4138
QY 3605 CUGUCAAGAAAUUUCUGUUAAGCAAGAGAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3664
Db 4139 UCAGGAUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 4198
QY 3665 CAUCCUGGACAUUUCGCGCAACAUUUUUCUGUAGGUGUGUUGGCGUUAUUAUUA 3724
Db 4199 UUCGCACAUCAGUGCAACAUCAUAGCUGCAUUAUUAUUAUUAUUAUUAUUAUUAUUA 4258
QY 3725 AGUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3784
Db 4259 AAUUCUGGAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 4318
QY 3785 CUUAUAUUCGUCACUAUUGCACAUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3844
Db 4319 AUAUGCUAUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 4378
QY 3845 UGAUAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3901
Db 4379 AGAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 4438
QY 3902 CAAAGAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3961
Db 4439 CGAUGGAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 4498
QY 3962 AUA-----AAGAUUUGCAAGAAAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 4012
Db 4499 AAUGCUUUGCUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 4558
QY 4013 AAAACUUGGAGAAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 4072
Db 4559 UGGAUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 4618
QY 4073 AAAGUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 4132
Db 4619 AGAGUGACUUGUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 4678
QY 4133 AACUUGCGCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 4192
Db 4679 GGAUGUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 4738
QY 4193 CCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 4252
Db 4739 CAGUGGACUUCGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 4798
QY 4253 UUGCCGCAUUGGUGGAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 4312
Db 4799 UUGAUGAAUUGGUGGAGAGAAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 4858
QY 4313 CUGGGAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 4372
Db 4859 AAGGGGUUUUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 4918
QY 4373 AUGCCCGGAGAAUUGGUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 4432
Db 4919 CAAUUAUGCAAAAGAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 4978

Db 7139 AAAAUCCAGGAAUUAUGCAUAUUGUCAAUGAAAUACAACAUGUCGACUCAAAAGUUG 7198
QY 6620 AUUUGCAACCAACAUAUCCUUAUUAUGCAUAUUGCAAAACAAAGGGAACAUAUGCAGGUGUUC 6679
Db 7199 AUCUUAACCGCACAAUCCACUACUUNGGAUGUGAAGAGAUAGACUAUUGCCGGUACU 7258
QY 6680 CUGAGAAGAGUUGUUGUUGCGACAAACGGAACAAGCAUAUAGCAUAUAGUAGAGAGGAAC 6739
Db 7259 CUGAAUAGAGAGUUGUUGUUGAGACAAACCGGACCCCAUAUAGAUAGACACUAUUAUGACG 7318
QY 6740 UACCGAAGCGAAUUGAAGAGUUGUUCUUU-----UGAAGGAGCCUCAAUGUGUGAAGG 6790
Db 7319 UGGCAGUGAAUCCUGAAGAGGAAAGUUAUUGGCGCAUGAAGUAAGUACUAUUAUCAGAG 7378
QY 6791 GAUUGCGCAUUAACAAGUGUUGAGCGAGCUUAUUGCCAAUCUACAACAACAUCUCAAUUG 6850
Db 7379 GCUUAAGGGAUUAACAACCAUAGCAAGGUGUUAUUGUACACCUAAUAGAAUGAAGGGAUG 7438
QY 6851 GUUGGUCCACCAACAUAUAGGGUUGCUUUGGCUACAUAUCAUAUUAUAGGCAU 6910
Db 7439 GGAGAAACAAGCAUUGCUUUGGAAUUGCGGAUACGGUGGUCUCAUUAUACAACAUAAGGCAUC 7498
QY 6911 UGUUUAAGAAAUAAUUGGGAUUAUUAUGAUCAAAUCCGACGCAUGGAAAUUUAUAUACA 6970
Db 7499 UUUUCAAAGGAACAUAUGGCACAUUAACAUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 7558
QY 6971 GGAAUCCCAAGCAAAUUAAGUGUGCGGAGUGGAGGAGUAUAGGAUUAUGCAUUCUCAA 7030
Db 7559 AGAACAACAACCCAAACUUGGGAUGAAACCUUGGCGUGACAGAGACAUACAUAUAGGA 7618
QY 7031 UGCUUAAGCAUUCACCAUUGGCAUUGGCAAGGUUACGAUUAUAGAAUCCAAUAGGUGUG 7090
Db 7619 UGCUUAAGGAUUAUACCUUGCUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 7678
QY 7091 AAUUAUUGUUGUUGUUGGAAUAUGCUUCAAAGAAAGUACAAUGCAAGCAUUGUUCUG 7150
Db 7679 AAAGAAUUGUUGUUGGUCAAAUUUAUUAAGACAAAUACAUAUUAACAAGCAUUCUG 7738
QY 7151 AGACAAGCAAAACAUAUCCACGAGUUGAAGGUAUUAUUGGAAACAUAUUGGAUUAUACA 7210
Db 7739 AAACUAGUACUAUGUACUGGCCAAACUACAUAUUAUUGGAAGCACUGGAUUGACGA 7798
QY 7211 CGGAAGCAUUGUGGAUUGCUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 7270
Db 7799 AGAUUGGCAUUGUGGCCUCCUUAUGAGUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 7858
QY 7271 AUAGUUUAUAGUACUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 7330
Db 7859 ACAGCUUGUCAAAUUAUGACAAAUACCAAAACUUGUUGCGUUCUUGGAGAAUUAUUG 7918
QY 7331 AAGGCAUUAUUAUUAACAAGUUAAGGAACUGAAAUUGGAGAGAGAAUUAUGGACUUAACA 7390
Db 7919 AAGCGAGUAUUAUGAGACUCCUGAGGCAUUGGAUUGGAUUAAGAAUUAUGGAGUUAACC 7978
QY 7391 UUAUAUCUAUUAUUGGGGCAACAUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 7450
Db 7979 CAGACGAAAUUUGUUGGGGAAACGUUGGAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 8038
QY 7451 AAACAACUAAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 7510
Db 8039 AAGUGUCCAAAACUGAUCACGGAUUAAGGAUUAACAAGUUAUUAUUAUUAUUAUUAUUA 8096
QY 7511 AAGUUAUGGUUAUUAUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 7570
Db 8097 -AGACAAUUGGGUCCAGGAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 8155
QY 7571 AUAACUUAUUAACAAGCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 7630
Db 8156 CGCAGUUAUGACUUAACAAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 8215
QY 7631 AAACUCGUAGUAGGCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 7690

Db 8216 AACAGACCAAUUCUGAAAGGGAUAUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 8275
QY 7691 GUUUAACAAGGAGCAUAUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 7750
Db 8276 GGUUUAUUAAGAGGCUUAACAUAAGGAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 8335
QY 7751 GGGAGUCCGACACUAGAGAUUUUUGAAGUUGCAGUUGGCGAAGCAUUAUUAUUAUUAUUA 7810
Db 8336 GUGAUGUCAAGUGGAUAUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 8395
QY 7811 AAUGGAAAUUUAUGGAAUUGCAAGUAUAUCAACGAUUGUGACAGAUUUUUAUUAUUAUUA 7870
Db 8396 CAAAAGGAUUCGAAAGUGUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 8455
QY 7871 ACAUAAAACCGCAGUUGGUGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 7930
Db 8456 AUAUAAAAGUUGCGUGCGCGGAUGUAACAGUGGAAGAAAGAAUUAUUAUUAUUAUUAU 8515
QY 7931 CCACAUAUUAUGAUCGAAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 7990
Db 8516 UGAGUAGAUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 8575
QY 7991 AUUUGGAAUUAUUGGAAUUGCAAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 8050
Db 8576 AGAAAGGUUCUGGAAUUGAUUCUGAAAGCGAGUUGAGACCCAUUAUUAUUAUUAUUAU 8635
QY 8051 CAAAACAACCGGRACAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 8110
Db 8636 UCAACAAGACAAAGAACCUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 8695
QY 8111 GGUUGCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 8170
Db 8696 GGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 8755
QY 8171 GGAUGCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 8230
Db 8756 GAAUUAACAAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 8815
QY 8231 UUAUCCGGAUUGGCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 8290
Db 8816 UUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 8875
QY 8291 CAGUUCUGGGAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 8350
Db 8876 CAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 8935
QY 8351 GAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 8410
Db 8936 GAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 8995
QY 8411 AAAAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 8470
Db 8996 AGAAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 9055
QY 8471 UCUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 8530
Db 9056 UUGUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 9115
QY 8531 AUGUCUGCAGGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 8590
Db 9116 AAUGUGUGUUCUUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 9175
QY 8591 UACAUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 8650
Db 9176 CCCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 9235
QY 8651 CUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 8710
Db 9236 CAUCCGGAACAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 9295
QY 8711 AUGACUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 8770
Db 9296 AUGGAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 9355

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|----|-------|--------------|-----------------|------------------|--------------------|-------------------|--------------|------|
| Qy | 8771 | GAAGUGUAAAAC | CAGAAAC | CACAGAUUAAGACG | GAUUTUGCG | UUCGCAUGA | UUGAAGCAUGGG | 8830 |
| Db | 9356 | GUUCACACGAG | CCUUAUUAUCUG | CACUGAAGCAAAUUG | UGCGCAAUUGG | UGGAGUGAUGGG | 9415 | |
| Qy | 8831 | GUUAACCCUAG | GUUAUCCAGAAUUCG | AAAAUUUUUAUUG | CTUGGGTUCUGG | AACAAAGCAC | 8890 | |
| Db | 9416 | GUUAUGAUGAA | CTUUCUUAUUAUC | AGAAAGUUUCG | AUCGCAUGGG | UGUUGGACCAAGGCC | 9475 | |
| Qy | 8891 | CAUACAACAU | CUVCUGCAUCUG | AGGGAAAGCCACAUA | CAUUUCGGAAAA | CAGCGCTCAAAA | 8950 | |
| Db | 9476 | CAUACAAGAAU | AUUAUCAGAGGUG | GAAGGCAUACAU | AGCTUGAAAA | CCGCACUCAAG | 9535 | |
| Qy | 8951 | GACUUUAACA | UGCGGAAGAGG | AAGUGCTUGAGAAA | UUAUGUAUCAUUA | UAGAGAGUGU | 9009 | |
| Db | 9536 | CACUUAACAC | UGGTUUAACCAU | CGAGUUAUUCUG | AACUGAGUGU | UAUACAAGAGUGCTUUA | 9595 | |
| Qy | 9010 | ----- | ----- | ----- | ----- | ----- | 9040 | |
| Db | 9596 | AUGAAUUGUA | CGAUGAUGUAU | UGCTUUCAGAGAAUG | AGUUGGAUGU | UAUCAUAUCUUG | 9655 | |
| Qy | 9041 | AUGAUGAAG | AUGUUUCACAC | AGUCCGCUUGAUG | CTUGCGAAAA | CCACAGCAGAAAAACA | 9100 | |
| Db | 9656 | GUGAGAAAA | CUGAAUUUAAGAUG | UGCGAGCAAA | CCUCCAGAC | CCUUAAGUCCAAAGUCA | 9715 | |
| Qy | 9101 | ----- | ----- | ----- | ----- | ----- | 9133 | |
| Db | 9716 | AUCCUCCACA | UAUACAAUAUC | UGAGAUUGU | UAGCGGAGGACCG | GAAGCAAGACGCTU | 9775 | |
| Qy | 9134 | ----- | ----- | ----- | ----- | ----- | 9184 | |
| Db | 9776 | UAAAGCGUG | CAGCAAAACA | CCCGCAACMAU | CCAGAUUAUUGG | CGGUGAUAAGA | 9835 | |
| Qy | 9185 | AAACUUCGA | UAUACGCAUCUG | GUGCUUAUUGU | UUCAAAACAGAA | AAAGAACAGAGU | 9244 | |
| Db | 9836 | GCAAGAAAG | AAUCAAUAGUG | GGAACAUCUAAAG | GGUGAGAGAA | AAAGACGUUA | 9895 | |
| Qy | 9245 | AUGUAGNUCA | AGUGNAUUTUCAUA | UACCAAGAAUUA | UUGAUUCCAUUA | CACTUCA | 9304 | |
| Db | 9896 | AUGUGGCA | CAGUUGGUAUUAUUG | UGUACACACGUGU | UAAGAUGAAUUG | CAAAUAAAGAAGA | 9955 | |
| Qy | 9305 | CAUUGCCAA | AGUGAAAGGAAAG | AUUUUAAUUGG | AGUUCUUUAUCAAUA | CACACAC | 9364 | |
| Db | 9956 | GACAA | CCAUUGGUAUGGA | AGCCAUUAUAAU | UUUCCACAUUGU | CAACAUAGAAC | 10015 | |
| Qy | 9365 | CAGAUCAUG | GAGCAUUUCAAUA | UACAGGCGCA | AGUAUUAUACAGU | UUUAUACUGGUA | 9424 | |
| Db | 10016 | CAGAGCAGUA | GAAGUUGGCAAC | CCCGUUCACCCAG | AGCAAUUCCAA | GAUGGUAUG | 10075 | |
| Qy | 9425 | ACGCTUGAG | AGGAUCCUUAUGG | UGUCUGAUGAGAA | UUGGAUUAUUGUAUGNAU | | 9484 | |
| Db | 10076 | AGGAGGUAA | AGGGGAUUAACG | UGUUGACACACAG | GAUUGGGGAU | CUUUAUGAUGAC | 10135 | |
| Qy | 9485 | UAAUGGUU | UGGUGUAUUGAAAA | UUGGAACAUUCU | CCAAAUAUAAUGG | CAUGUGGUUUAUGA | 9544 | |
| Db | 10136 | UAAUGGUU | UGGUGUAUUGAAAA | UUGGCAUCCCAAAUUA | AAUAAUUGGUGUGG | GAGAAUUA | 10195 | |
| Qy | 9545 | UGCAAGGGG | AAAGAAACAAU | UCGAAUAUACCC | CTUACCAUUGUGG | AAAAACCGAACCA | 9604 | |
| Db | 10196 | UGGACGGUGA | CGAGCAAGUGACAUA | UACCAUUAUAAAC | GAUUGUUGAUAUG | CAUGCAGUGCTUA | 10255 | |
| Qy | 9605 | CUUUGCGU | CAGAUUAUGG | CTUCAUUAAGCAU | AGUUGTUGAAGCAUA | UCUGAAAGAGAA | 9664 | |
| Db | 10256 | CUUUUAGG | CAGAUUAUGAC | GCACUUCAGUGA | CGUUGCAGACCU | UAUUAUAGAAUUGCGAA | 10315 | |
| Qy | 9665 | AUUAUGAGA | AGCCAUUAUUG | CCGAGGACGGAUUA | UUAACCGAAACCTU | CACCGCAUGAGU | 9724 | |
| Db | 10316 | ACCGUA | CAAAAGCGUAUG | CCCAAGAUUGG | UUAUUAUUAUUGA | UAUAGUAGU | 10375 | |
| Qy | 9725 | UGGGCGAU | AUGCUUUUGAUU | UUCUAUAGAA | UAGCAUCAAAGG | ACGCCAGCUGGGCCGGG | 9784 | |
| Db | 10376 | UUGCGGGAU | AGCAUUGAUUUUA | CGAGCUGCAUUA | CAACACUGCA | CGUGCUAAAG | 10435 | |

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| Qy | 9785 | AAGCCCAUCCAGAGUAGAAGCTUGCGAGCAUUGCGAGAUUAGAAUAGAUGUUUGGAC | 9844 |
| Db | 10436 | AAGCACAUUUACAGAUAGAAGCGAGCGGCACUUAAGAAUUGCGGAAUUCGGUUUUGGUU | 10495 |
| Qy | 9845 | UGGAUGGAAAAGUCGGAUUAUGCGACUGAGAACACGAGCGCCACACCGCAGACGAGUUA | 9904 |
| Db | 10496 | UGGACGGAAGCGUCCACGCAAGAAGAAGAUACGGAGGCGCACACACUACUGAUUA | 10555 |
| Qy | 9905 | ACCAUACACUCAU 9918 | |
| Db | 10556 | CUAGAAAUACAU 10569 | |
| RESULT 4 | | | |
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| ID | AAC64469 | standard; DNA; 9584 BP. | |
| XX | AAC64469; | | |
| DT | 13-FEB-2001 | (first entry) | |
| XX | Clover yellow vein virus gene SEQ ID NO:1. | | |
| DE | Clover yellow vein virus; gene expression; plant; GFP; | | |
| XX | green fluorescent protein; environmental stress; ds. | | |
| KW | Clover yellow vein virus. | | |
| OS | JP2000245469-A. | | |
| PN | 12-SEP-2000. | | |
| XX | 26-FEB-1999; 99JP-00051762. | | |
| PF | 26-FEB-1999; 99JP-00051762. | | |
| XX | (HOKK-) HOKKAIDO GREEN BIO KENKYUSHO KK. | | |
| PA | (HOKU-) HOKUREN NOGYO KYODO KUMIAI. | | |
| PA | (UEDA/) UEDA I. | | |
| XX | WPI; 2000-667343/65. | | |
| DR | A gene expression vector for plants. | | |
| XX | Example 1; Page 8-12; 16pp; Japanese. | | |
| CC | The present invention describes a gene expression vector for plants of | | |
| CC | the Lemnaceae or Nictotiana genus of Solanaceae or the gladiolus genus | | |
| CC | of Iridaceae, comprising a cDNA against the genome of a clover yellow | | |
| CC | vein virus. Also described are: (1) a bacterial host transformed by the | | |
| CC | gene expression vector in a plant; and (2) a transformed plant in which | | |
| CC | an exotic gene is introduced by the gene expression vector into a plant. | | |
| CC | The gene expression vector can be used for creating a useful plant highly | | |
| CC | resistant to environmental stresses. The present sequence represents a | | |
| CC | clover yellow vein virus gene which is used in an example from the | | |
| CC | present invention | | |
| XX | Sequence 9584 BP; 3195 A; 1713 C; 2210 G; 2466 T; 0 U; 0 Other; | | |
| SQ | Query Match 20.6%; Score 2093; DB 3; Length 9584; | | |
| | Best Local Similarity 39.0%; Pred. No. 0; | | |
| | Matches 3291; Conservative 1273; Mismatches 3760; Indels 105; Gaps 11; | | |
| Qy | 1581 | UGCAGGUUUGAGUUUGGAAAGGUUUUGAUCGUCUAUUUUGACUUCGAGUAGACC | 1640 |
| Db | 1099 | TGCAGGAGATTGTTTGGAAAAGGTACAAATCAGACTTTCTAGATAATAGACCAAAA-- | 1156 |
| Qy | 1641 | UAGAAGCGCUACGAGUCGAAAGCCCAUAUAAACGUGAGGAGUGGCGAAUUGGCAGC | 1700 |
| Db | 1157 | -GACATTTGNACACACGTGTACATCAGATCTCAATGTAATTCATGTGGTCTGTGATGCG | 1215 |
| Qy | 1701 | CAUUGUAAACCAACUCCUAUUUCCAAUUGGAGAAAAUAAACUACUCUAUUGGAGAAACU | 1760 |

Db 1216 GTTGATGACTAGCACTATTCCCGTCGGAAGAATCACTTGCAAGAATGTGTGGAGGA 1275
QY 1761 GCUGAAUUGUGUCACAGAGAGAGAAUCUGAAUUCUUCAGCGCUAAAGAGAGCAAUU 1820
Db 1276 TTTTCATAATCAGAACAATAGGAGAGATATGCAAGAACAGAAAGATTTTTAAGCCAGGC 1335
QY 1821 GGCAAGUAAAUUUAUCCAGUCUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 1880
Db 1336 AATGACTCTCTAGCAACAACATACCAGAAATTCAAACACTCGAGAGACATCTTGCAATT 1395
QY 1881 AUUAGAGAAUAGUCUGAAUUGGAGUAGAACAAACAACUUCGUAUGGCGCAACAACAUAUGCACA 1940
Db 1396 GTTTCGTGAGCGTTTAAGTATGGAACCTCAAAATGCAGAGGCGTGTGTGAGACAAACAA 1455
QY 1941 AAUUAUUGCGAGUCGCAAGAGAGAUUCUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 2000
Db 1456 AGCCATAACATCACTTTACAGAGACTCCATTTTAACCATAGAGAGATAAATGAGGTGCT 1515
QY 2001 AAUUAAGUCGGAAUAAACUUUUAUGCGAGGAUUUAUUAUUAUUAUUAUUAUUAUUAUUA 2060
Db 1516 TTTAAGATATGTTAGCTGCACAAATGATGAGGTGGGGTTGCAAGTGCAGCTTACTTGA 1575
QY 2061 GCUAACACGCGUGGCAUAAACAGGAGCGAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 2120
Db 1576 AATTACTAGGTACATTCGAAACAGAACTGATTCATCCAAAGGAATGACCTAAGTAAGTT 1635
QY 2121 CGGAAUAUAGUUCAGAAAGCAAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 2180
Db 1636 CAGAAACAAGATTTCTCAAGAGACACATCAACCTAGATTTAATGTGTGTAACCACT 1695
QY 2181 UGACAAAAUUGUUAACUUGUGUGGGUGAAAGAGUUAUUAUUAUUAUUAUUAUUAUUAUUA 2240
Db 1696 TGACAAAATGCAAACTTCATGTGGGGTCAAGAGCATACCATGCAAAACGATTCTGTGC 1755
QY 2241 AAACUUUUUGAGAAUUGAUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 2300
Db 1756 GAATTTATTTTCAGTGTGATTCATCTGAAAGTTACGACAAATTCATCAATAGAAAGTT 1815
QY 2301 CCCAAUGGCACAGACAAACGUAUAGGAAACUGAUUUUAUUGAGCGAUCCAUUAC 2360
Db 1816 ACCCAATGTGACAGAGAACTTGCAACTGCGAGGTAAATGTGCTTACAAACTTTGGAATC 1875
QY 2361 GCUACGACAAACAAUUGAAAGUAGCCAAUFCACAGAGUUCAGUUGGUUAAUUAUUGUAC 2420
Db 1876 TTTTAGAGATCAATGAAAGGAACCATGTGTGACATAGACCAAATTTGGCAAGAAATGTGT 1935
QY 2421 AAGCAAAAGAGUUGUUAUGUCUUAUCCAGCAUGCUGUGUUAUUAUUAUUAUUAUUAUUA 2480
Db 1936 TTGCGCGTGTAAAGGAGCCCTTTTGTACCGCTGCTGTGCACAACTGATGATATTGGCAA 1995
QY 2481 GCCAUUUGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 2540
Db 1996 TGCAAATTTGTCTGAAATTTAAATGCGCAAAATATCATTTAGTTCTTTGGTGGTCAGGA 2055
QY 2541 AGAUCCAAAGUUAUGGUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 2597
Db 2056 AGCAGCGAAATACATAGACTACCATCAGATGAGTGGCATGATGATACATAGCAAAAGA 2115
QY 2598 AGGUUAUUGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 2657
Db 2116 TGGGTATTGCGCATPATTAATATATCTTTCTGTATGTTGTTGTTGTTGTTGTTGTTGTTG 2175
QY 2658 AAAUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 2717
Db 2176 AAAGGATTTTCAAGAAATGTTGGGGGATCAGATAATGCCAAAGTTTAGGTACGTGGCCAA 2235
QY 2718 CUUUAUUGGUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 2777
Db 2236 AATGCTAGATGTTGCAACAGCGTGTGGTACTTAAACAGTTTGTGTTCTCTGACACACTCAG 2295
QY 2778 UGUGAGUUGCCCCGAAUUCUUAUGUAGUACUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 2837
Db 2296 TGCTGAACCTTCCAAGAATACTTTGTTGATCACAAGTTTAAGCACCAATGACAGCTTCTGGATT 2355

QY 2838 AUUUGGCUUCGACAGACGCAAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 2897
Db 2356 GTATGTTTCATAAGCACAGGATACCATGTTCTTAAGGCAACATTTGTTCCCAATTAAAT 2415
QY 2898 UAAAUUCCGCCAUUAUGAUUUGGUAUUCGAGCUGAGAAACAUUAUUAUUAUUAUUAUUAU 2957
Db 2416 CAAATTTGCCAGTGCAGATCTTGAGTCAGATTGAAGTTTTCACAGATTTGGTGGCAATC 2475
QY 2958 CCAUAGCAAGCAAGCUCUCAGUGUUCCAUAAAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3017
Db 2476 ATTGACAGGGCAGGTGATACAGTTTGACACAAAATGTTAATCTCAAGTATTTTACCGAC 2535
QY 3018 UAAAUUAUGAGGCAAAUUAUGAGGAAGAGCCUUUUUUUUUUUUUUUUUUUUUUUUUUUU 3077
Db 2536 AAGGCAGATGGAAGAAGATCATCAATGAAGAACATTTGTGTAGTTCTTAGCAATGCAGTC 2595
QY 3078 ACCAGGUGUUUAUUAUGCUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 3137
Db 2596 ACCATCAGTTCTTCTGGCCCTATTTCATATGTCCTCGCTAGAGAAAGCGTGGAGGTTTG 2655
QY 3138 GAUAGAGCAAGCAACAGUCUCUGUGCUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3197
Db 2656 GCTGCACAAAGACATGCGTGTCTCACATGTGATGACAAATGCTTGCCCTCTTGGCAGCAA 2715
QY 3198 AGUAAACAGUUCUAAAAUUAUGAUGAGCAGAGACUAAUUAUUAUUAUUAUUAUUAUUAUUA 3257
Db 2716 AGTAAGTCAGCTAAATGTTGAATTTACAGATGGAATAATTTGAAGCTAGTGTGGCCA 2775
QY 3258 UUGAUUUUGGUCUUGGAAACCAUACACAGCAAGCCAUUAUUAUUAUUAUUAUUAUUAUUA 3317
Db 2776 CTTTCTCGCTGCAATGGACACCAATTCATAAGCCAATGCATCCATCAACACAGCAAAACAT 2835
QY 3318 UCAACUACAGGUCAGGCAAUCCUAGAGACAUAAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3377
Db 2836 TTTCTTGTATGAACCTTGGAAAGAGGGAGATCGACTGACAGAAACAATTTGATGAATTTGGGTT 2895
QY 3378 CAGCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3437
Db 2896 CCATCTTTTGAAA---AAGTCTAGTCAAGTACTCATGGAATAATCTGGCGCAGAGGATTT 2952
QY 3438 AGAGAUUUGGAGAACGACUUAAGUGUGGUAAGAAAUUAUUAUUAUUAUUAUUAUUAUUAU 3497
Db 2953 AGAGCAGCAATGGCTAGGTTTAAAGATTGTCACAAAGTTTATTTAATAAAGCAGTCATG 3012
QY 3498 AAAAUACUAAUUAUUGGUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3557
Db 3013 GAAGCAGCGGGCAAGATATTCAAAATACTAGCCAGAGAGACGAGCTAGGTGGCAGCA 3072
QY 3558 UCGAUUAUUCAGUUAUCUGCAAGCAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3617
Db 3073 CAAGTTTCAGCGCATCACTCAGATTGTTCAGTAACAGCATTAAAGATCAAGCAATCAGTTG 3132
QY 3618 UUGUUAUAAAGCAAGAGAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3677
Db 3133 CAAGAAGAGAAATGGTCATCAACAAGTAAGAAATGTTTGTTCAGTGTGCGAATAATGTTGGC 3192
QY 3678 UCGGCGCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3737
Db 3193 AATACAAGCCTTTAAGAGTGTTTAAGCGATGATGATGATGATGATGATGATGATGATGAT 3252
QY 3738 GCUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3797
Db 3253 GCTAGCAACAATTACGCTCCTGATGGGCATTTCTGAGTCAAGTGAATCTCATCAATAAC 3312
QY 3798 CUUAGCAAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 3857
Db 3313 TGTCAATCATACAGCGCTTTTCGAGAGAAAGCCAAAGTCCAAGATGATCTGTACA---G 3369
QY 3858 AGUGGCCCUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3917
Db 3370 AATCAATGATTATGATGTTGTTGAAGCTCGTGATAGGTACACAGTGGATGATGTTGCG 3429

QY 3918 GGAGUACAUUGCAAGAGUAGACCUGAGCUGAUUGCAUUGAUUUAUAAUUGCAAGA 3977
Db 3430 CAGTAAGCTGGAATCACTAAACCCAGAACTCTAGAAACTTTTCGATGATATTACAAGGA 3489
QY 3978 AGAA-----GUUGAUCAUCAAGCUGAAGCCAAAGGUGUACAACAAUUGGAGAAAUU 4031
Db 3490 ACCAAAGTGGTTTGTCTATGGAATCCAAATCAAAATGACATGGTGGCTCTTGAAGAAAGTAGT 3549
QY 4032 AGCAUUGUUGCCUUAAGUUAUGAUUUUUGACUCAGAGAAAGAUUGAUUUAUUA 4091
Db 3550 GGCTTTTACAGCACTCGTTATGATATATTTGATGGAGAGAGATGACTGTGTATTACAA 3609
QY 4092 GACACUGAAACAAUUGCGAAUUCUGUUGCCACAUUGUAGAACCUUG---UCCGCAUCA 4148
Db 3610 AATACTGAATAAGCTCAAGGCGATAATTTCAACAACTCAAGACGGCTACAAATTTCA 3669
QY 4149 AAGCUUGAGCAGCAUUCAGACAUUCUGACUGACGACCAAGAAACAAACAUUGAUUUCGACUU 4208
Db 3670 GAGTCTTGATGACATTAAGCCTATGTTTGAAGAGCAAGAGGGTGTCAATTGATTTGAGAT 3729
QY 4209 AGAUUGAGGGGAGCAAGAUUACAGAGUUCUUAAGGAGAUAAUUCUUGCCGCAUGUGGGA 4268
Db 3730 TGATGAGGGTGACAGCAAGATATATGCAGCAACCAACCAATTTGTTCAATGGTGGGA 3789
QY 4269 AAAACAAUACAAUUGAUAGAGUGGUACCCCAUUAUAGAACCAUUGGGAUUAUUAUGA 4328
Db 3790 CAATCACTTTCAGAAATGGGAATGTCTACACACTACAGAAACAGAGGGTCAATTTCTATGA 3849
QY 4329 AUUCACUGUAGAAUGUGUUAUGUAGUGAGUUAACAAUUAUCUACUUGCCCGUUAAGA 4388
Db 3850 GTTTTACCAGAGATACAGCAAGAGGTTGCGCAACAATAGCCCAACAGTGAATTTCAAAGA 3909
QY 4389 AUGGAUUGCCGUGUGUGUUGAUUGACAGGAAAUUACUUGGUUACCAUUCGCGUUAUC 4448
Db 3910 CATTTTGTAGAGAGGGCTGTGATCAGGAAATCGACTGGCTTACCATCATACCTTAG 3969
QY 4449 UAGUAAAGGCGAGUUCUUAUGCUGAACCAACAAGACCAUUGGCGAGAGAAUGUCUACG 4508
Db 3970 TGAAGAAAGGAAGTGCTGATGTTGGAGTCAACAAGGCCGTTAGCAGAAATGTTTCAA 4029
QY 4509 ACAGUUGAGACAACUCCUUUAUGCAACCCCAACUUGAGAAUGCGGAGGAUUGUACUC 4568
Db 4030 GCAGCTCAAGAGTGATCCCTTCTACAGAAACCCCAACTTCGCATGAGAGGAACAACGAG 4089
QY 4569 UUUUGAUUAGUAAUUAUUGAUUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGU 4628
Db 4090 CTATGTTTCAACCAATTAATCATATTCATAATCATAGATGAGTGCATGTTCTAGA 4149
QY 4629 UAAUCCUCUAAAAUUAAGUAGUUAUUGAUUUGAUUUAUAGUAGUAGUAGUAGUAGUAGU 4688
Db 4150 CAACCTCTAGTTACTGAAAGAGTTCCAAATTCATAATCATAGATGAGTGCATGTTCTAGA 4209
QY 4689 UAGCAAGCUUAGCAUUCUGUGUUCUUCUCAAAGAAACAAUUAUGUAGGCAAAUUAU 4748
Db 4210 TGCTAATGCAATTTGCTAGTTTGTCTCAAGGAGTTTTCATTTTCAGGGGAAACTTGT 4269
QY 4749 GAAUGUAGUAGCAACCAAGGCGGUGAUUUGAUUUGAUUUGAUUUGAUUUGAUUUGAUUUG 4808
Db 4270 CAAAGCATCAGGACACCAAGAGAGAACTGAAATTCACACACACACACAAAGTGTCT 4329
QY 4809 CAUUCAUUAGAGGAAACAAUUAUUGUUCUUAAGCUUUUUGUAGAGCUUACAGGAA 4868
Db 4330 ATGGTAAACCAAGACCACTTTCTTTGATCAATTTGTTGGCCCGCAGCAAGGTACAGGTT 4389
QY 4869 UGCACGAGUUAUUAUUAAGGAGACAACAUUUUAUGUUAUGUUAUGUUAUGUUAUGUUA 4928
Db 4390 CAATTTGGCATGATGTTGTGTCGCACAATATCTGTTATATGTCGCGAGTTACAAATGA 4449
QY 4929 GGUUGAUCUCUCAAUUAUGUCCGAGUUAUAGGCUUUAUUAUGUAGUAAAGUCCGAGUG 4988
Db 4450 AGTGGACCGCTTTCAAAGATGTTACTGGGAAAGGGTCTCCTAGTGACGAAAGTGCATGG 4509
QY 4989 GCGUACCAUAAAAUUGGUUCGACCGACAUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 5048

Db 4510 GAGAACCAATGAAGAGGAGAAAGACTGAGATTGAAACGAGGGGACAAAAGCAAAAGCA 4569
QY 5049 UUUCAUUGUAGCAACCAACAUAAUUCAGAAUUGGAGUCACUCUAGAUUAGUUAUGUUAUGU 5108
Db 4570 TTTTGTGTTGTCACAAATATCATAGANATGGAGTAACTGCTGATATAGAGGGTGTGT 4629
QY 5109 GGACUUGUUGUUAAGUCACUCUGGAAAUUGAUUACGAAACCGGUGUGUUAUUAUACAC 5168
Db 4630 AGATTTGGGTTGAAGTTGTTCTGAGTTGACGCGCAGATAGCAGGGTGTATGCGCTATTTC 4689
QY 5169 AAAGACCAGCAUUCUACUACGAGAAACGCAUACAAAGAUUGGCGGAGUUGUAGACACA 5228
Db 4690 AAAGCAGCAGAGTTTCATTTGGTGAAGAAATTCAGAGAATTTGAAGAGTTGGCAGGCA 4749
QY 5229 GAAAGGGCAUGCAUUGAGAAUUGGAAUUAUUAAGAUUUGAUUUGAUUUCUAGUCU 5288
Db 4750 AGCTGTAAGCACTCAAAATTTGTTACACAGAGAGAACTTTCAGAGATCCAGAAAT 4809
QY 5289 UGUGGCGACACAGGCGUCAUUAUUGCUUACAUUAGAUUUGCCUGUUAUAGACACAAG 5348
Db 4810 GGTGCGCTACAGAAAGCAGCATTTCTATGCTTTGTCATATGGCTTCCAGTCTATGCTGAGG 4869
QY 5349 AGUUCAGUUAACAGUUAUUAUUGACAGUCCGACAGGCGCAGAGUUAUUGUCUGUU 5408
Db 4870 AGTGTCTCTCAACATGCTGAGTAAATGTACAGTACGCAAGCCCAAGCCATGATGAGCT 4929
QY 5409 UGAGUUGCGCCUUAUUCUUAUGCUUACUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 5468
Db 4930 TGAATACCAATCATGTATGACACAGTTAACTTGTGTTAGTTTACGGTTCATATGATCCATC 4989
QY 5469 AAUUCACAGCAAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 5528
Db 4990 CATACATGAGTTACTTTAAACCATACAAAGCTGAGGGACTCAATGTTGTTTAAACAAAT 5049
QY 5529 GGUUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 5588
Db 5050 GGTATACACATGAGGAGTGTCAAAACTGGAATTTTCAGTCAGAGAGCTCAAAATATGTTGG 5109
QY 5589 AAUCCAUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 5648
Db 5110 TGTAGATTGATATTCAGAGAGACATCCGAGTGCCCTTCATGCCAGAGATATACAGA 5169
QY 5649 UAUGAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 5708
Db 5170 CAAAGTTACATGAGAGGATATTCGAGGCTTGTGAAGACAAAAGGGGATGCGAGTTTGG 5229
QY 5709 UAGAAUGAGUUGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 5768
Db 5230 AAGACTCAGCGTGGTTAGTGCAATGCAAGGTGCTTACACTCTACAAACTGATCCTACATC 5289
QY 5769 AAUUGGAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 5828
Db 5290 ACTGCAAGAGACGATCAAAATCCTGATGAGTTAATAGCAGAGAAACAAGGAAAGAGA 5349
QY 5829 UCAUUUUUAAGCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 5888
Db 5350 GTACTTCCAAAGTGTCTTCAACACAGCATGCTCTGCTGCTGAGTTACTCTCTGACGAGCAT 5409
QY 5889 AGCAAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 5948
Db 5410 CATCAACGCAATTAAGGCAACGCAACCTGTGATTTTCAACCAAGAAACTTGTAGCGTGTCT 5469
QY 5949 GCAGGCGACAAAGAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 6008
Db 5470 ACATAGTGTAGCAGCAACTGATGAGATTCAGAAACATTAATGATTTGATTTCTAGACC 5529
QY 6009 AUGCGGAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 6068
Db 5530 ATCAACACTTGTAGTGTGTTGGTGCATGAGTGTGTTGAGTGTGTTGAGTGTGAGTGTGAT 5589
QY 6069 UUCAAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 6128

| | | | |
|----|------|---|------|
| Qy | 8274 | ACCAUAUUCUGAUAUGCAGUCGCGGAUUUAGGAAUUGGGAUUGGGACAUC | 8333 |
| Db | 7810 | ACCATTCCTGATAAATCTGTCTTGAGACTTGCAGTCAACTTTGGAAGAGTGGGCACAT | 7869 |
| Qy | 8334 | AGCGGUCGAGAUGCUCUGAAAUIIUGGACACUCAGAAUAUUAUACACCCCCAUUGCACACC | 8393 |
| Db | 7870 | TGGTGAGGAATGCTTAAGAACTTGTACCGGAGATCATATATACCAATCTCTTAACACC | 7929 |
| Qy | 8394 | UGAUGGAAACAGUCGCUAAAAAGUUUCGAGGAAAAUAAUAGUGGUCAAACCGUCAACAGUCGU | 8453 |
| Db | 7930 | TGATGGTACAATAATCAAGAAGTTCAAAGGGAAACAACAGTGSACAACCATCGACAGTTGT | 7989 |
| Qy | 8454 | AGAUNAACAUAUGAUGGUCUGAUUUUGUGUGGACGUAUAGUUUUUAUUAUAGUAAGUGUAAA | 8513 |
| Db | 7990 | CGACAACAACATAATGTGTGATAATGGCTATGTACTATGCAGCAAAAACTTGTGTGT--- | 8046 |
| Qy | 8514 | GUUUGAGAAUUCAGGAUGAUGCUCGACGUAUUCUGUUAACGGUGAUGAUUUUUGUCUUC | 8573 |
| Db | 8047 | GGAAGGAGATTAAAGCGAGTCCATTGTGTCTACGCCAATGGTGATGATTTGTTGATAGC | 8106 |
| Qy | 8574 | AUCAAUCCAAAAUUUAUACACAUCCUAGAUUUUUUAAAAGUUAUUGUCAAUUUUAUUGG | 8633 |
| Db | 8107 | AGTGACCCAAGTCATGAGTGTATCTAGACCAACTTCTTACACTTTTCAAAGATTGGG | 8166 |
| Qy | 8634 | UUUAGACUAACAUUUCUCAUCGAAACGAAAGAACAAAGAGAAACUUUGGUUUUAUGUCUA | 8693 |
| Db | 8167 | C TTGAAC TATGATTTCTCAAGCAGGACAAAGAAATAAAGSTGATCTCTGGTTTCATGTCA | 8226 |
| Qy | 8694 | CAAAAGGAGUAAAUAUUAUGACUUAUUCUCAAAGCUGGAGCCAGAGAGGUGUUCUC | 8753 |
| Db | 8227 | CTGTGTATAAAGAAAGAGTTTGTGGATTCCCAAGTTGGAGCCAGAAAGATGAGTCT | 8286 |
| Qy | 8754 | AAUAUUCUGAGUGGAUAGAGUGUAAAACAGAAACACAGAUUAGAAACGUAUUGCGCUUC | 8813 |
| Db | 8287 | AATCCTTGAATGGGATAGAGCGGCAGAGCCTGAACATAGTTGGAAGCTATTTGTGCATC | 8346 |
| Qy | 8814 | GAUGAUGAAGCAUGGGGUUAACCUAGUUUAUCCAGAAAUUCGAAAAUUUUAUUGCUUG | 8873 |
| Db | 8347 | CATGATCGAAGCTTTGGGGTTATGATGACTTGTGCTCAATCACAATACCGCAGTTTTTATG | 8406 |
| Qy | 8874 | GGUUCGGAACAAGCACCAUAUUAUUCGCAUCGAGGGAAGGAGGACCAUAUUAUUC | 8933 |
| Db | 8407 | GGTTCTTGACCAAGCACCATACAACAGCTCAGCGCAGAGGAAGAACCCCTATATCTC | 8466 |
| Qy | 8934 | GGAAACAGCGCUAAAAAGACUUUAACAUCGAAAGGAAGGAGUGUAUAAUUAUUGC | 8993 |
| Db | 8467 | AGAAGTTGGTTGAAGAGTTGTATACCTGGGAACACAGCTACAAGTTGTGAACTAGAGT | 8526 |
| Qy | 8994 | AUACUUAAGAUUGUGCAUGUAUUGAACGAGGAUGAGUACUUUGAUGAUGAAGUUG | 9053 |
| Db | 8527 | GTAACAATAAGATCCATCAAGAGCAGCAGATGAGTTTGTATGACAGCCAGATGAAATTTGT | 8586 |
| Qy | 9054 | UUCUCACAGUCGCGCUCUUGAUGCUGGCAACCCACAGCAGAAAAACAAAGAACAGCAUGA | 9113 |
| Db | 8587 | TT-----TCCAATCCCAACAAGAGAGTTGAATGTTTGGTGAAGCAACAAAGTCAAGGATAA | 8643 |
| Qy | 9114 | AGAGAGAAAGAAUAAAGAGAAAAAGCAGGAAAAUAAAAACAAAAUAAAGAUUCGAGAA | 9173 |
| Db | 8644 | GGAGTCAAGACAAGAGATCAAGAGGGTGAANAATCTAACA- | 8684 |
| Qy | 9174 | GAACAUGAGAAAAAUUCGAUUAAGCGCAUCUGGUGUAUUGUUUCAAACAACGAAAAAGA | 9233 |
| Db | 8685 | -----GACAAATCATTTCCAGA | 8700 |
| Qy | 9234 | CAAGGAUGCGAUGAUGAUCAGUGAUCUUUCAUAUACCAAGAAUUAUUAUUGCAUUC | 9293 |
| Db | 8701 | CAGAGACATCAATGCAGGAACCACTGGGACTTTTTCAGTAGTACCCCAATTGAAGAAAAATC | 8760 |
| Qy | 9294 | CAAUAAACUCACAUAUGCCAAAGUGAAGGAAGGAUUUUUAAAAUUUGGAGUUCUUUU | 9353 |
| Db | 8761 | AGNAAGCTTTCTGCCCCAAAATCAAAAGGAAGAAGHACTGCTGAACTTTGGACCACTTGT | 8820 |
| Qy | 9354 | ACRAUACACACAGAUCAAGUGGACAUUUCAAAAUACCAAGGGCAAGUAUUUACAAGUUUAA | 9413 |

[illegible]

Db 4741 AATAAAACACTGGTTGAATTCAGAAATGGTTGCCACTGAAGCTGCCTTCTATGCTTC 4800
QY 5320 ACAUUGGAUUGCCUGUAAUGACAAGAGAGUUUCAGUUUAACAGUUUAUCAAUUGCACA 5379
Db 4801 ATGTACAAATTTGCCAGTGACAACACAGAGTGTTTCAACCACACTGCTGGAAAATGCCACA 4860
QY 5380 GUCCGACAGCCAGAGUUAUGUCUUGUUUGAGUUGCCCUUAUUUUGGCUUACU 5439
Db 4861 TTATTACAAGCTAGAACTATGGCAGAGTTGAGCTATCATATTTTACACAATTAATTTT 4920
QY 5440 GUUAUACAUGAGGCGACAGCAACCCUGAAAUUUCAAGCAUUAUUUUAUUAUUAUUA 5499
Db 4921 GTGCGNATTTGATGGTAGTATGATCCAGTCATACATGACAAGCTGAAGCGCTTTAAGCTA 4980
QY 5500 GAUGAAUCUGAAAUCAAUAUGUGCCAUUGGUUUUAUUAUUAUUAUUAUUAUUGG 5559
Db 4981 CACACTGTGTGAGACATTCCTCAATAAGTTGGCGATCCCAATAAAGGCTTATCCTCTTG 5040
QY 5560 CUAGAUGUAUUUAUUGACAGUAUAGAAUCCAUUUAUUAUUAUUAUUAUUAUUAUUA 5619
Db 5041 CTTACAGTGGAGAGTATAGCGACTTGTGTATACATAGCAGAGGATGCTGGC---ATAAGA 5097
QY 5620 AUUCCAUUCCAUUGUAGAAUUAUCCAGAUUAUGAAUUAUUAUUAUUAUUAUUAUUA 5679
Db 5098 ATCCCATTCGTGTGCAAGAAATTCAGACTCCTTGCATGAGAAATTTGGCACAATTGTA 5157
QY 5680 CUCAAAUUAAGACAAUUAUUUUUUGUAGAAUAGAGUUUUGAGCGCAACAAAAGUA 5739
Db 5158 GTCCGCCATAAAGTGACTCGGTATTTGGAAGGCTCACTAGCGTACAGGACGAAAGGTT 5217
QY 5740 GCUAUACACUUAACACACAUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 5799
Db 5218 GTTTATACTCTGCAACCGATGTGACTCAATTTGCGAGAGCTCTAGCATGCATCAATAGA 5277
QY 5800 CUUUGCAAGAAUUAUUAAGAAACAGCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 5859
Db 5278 CGATAGCAGATGAACAAATGAAGCAGAGTCAITTTGAAGCCGCACTGGGAGAGATT 5337
QY 5860 AGUGGAAACAUUUUUAUGUUAAGCAUAGCAUAGCAUUAUUAUUAUUAUUAUUAUUA 5919
Db 5338 TCCTTCACAAATTTACTCAATACAAAGCATATTTGACACGCTGAAGCAAAATTTATGCTACA 5397
QY 5920 GACUACACUGCGCAUUAUUCAGAAUUGCAGGCGAGCAAGAAUUAUUAUUAUUAUUAU 5979
Db 5398 AAGCATACGAAAGAAATATTCAGTGCTTCAGCAGCGCAAAAGATCAATGCTAGAGTT 5457
QY 5980 GUCAUUUAUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 6039
Db 5458 TCGNACTAGCAAGGATCAAGATGTCACGGTATATCATCAAGACTTCAATCACCTGGNA 5517
QY 6040 CUAGUUAUCCUACAGAGCGGCAAGAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 6099
Db 5518 ACTATCTATCTCAATCAGATACGGAAGTGGCTAAGCATCTGAAGCTTAAAGTCACTGG 5577
QY 6100 AAUAGUCACUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 6159
Db 5578 AATAAAGCCAAATCATCTAGGACATCAATAAGCTTTGCTGTGTTAATTTGGTGGGA 5637
QY 6160 UGGAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 6216
Db 5638 TGGATGCTTGCAAGTACTTCAAGGACAGTTCATGAACCGACTTATTTCAAGGGAG 5697
QY 6217 AGGA---AGACUCAAAGCUUAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 6273
Db 5698 AAGAAATCAGAAGCACAAGCTTAAGATGAGAGAGCGCTGGGCTAGAGGCAATATGAG 5757
QY 6274 GUUAUUGGAGCAGCGUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 6333
Db 5758 GTTGCAGCGGAGCAGAGGCGCTAGAACATTTACTTTGGAAGCGCATATTAATACAAAG 5817
QY 6334 GCAGUUAAGGCCAGAGAGAGAAUUGGCGCAAAAUUAUUAUUAUUAUUAUUAUUAUUAU 6393

Db 5818 AAGCGAAGGGCACCAACAGAGAGGAATGGGTGCAAAAGTCTCGAAAATTCATAAACATGTAT 5877
QY 6394 GGAGUUAUUUAAGAAUUUUUGUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 6453
Db 5878 GGGTTTGATCCAACTGATTTTTCATACATTAGGTGTTGGATCCATGACAGGTCACACT 5937
QY 6454 CGUGAUGAGAGUCCUUUGACAGUUGGAUUUAGUUAAGCUCAUUAUUAUUAUUAUUAUUA 6513
Db 5938 ATTGATGAGTCCAAACAGCACCTATTGATTGATGAGCATGAGTTTGGAAAGGTAGA 5997
QY 6514 GACAAAUUGCUAAGCGAGGCGCUCAUGAUAGGCAACAACAUCUUAUUAUUAUUAUUAUUA 6573
Db 5998 ACAGCATGTTAATTGACGATGAGTAGAGCCTCAAAGTCTTAGCACCCACACCAATC 6057
QY 6574 ACAGUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 6633
Db 6058 CATGCTTATTTGGTGAATAGTGGCAGGAAGAAGTTCTTAAGGTGATTTAAACCAACAC 6117
QY 6634 AUUCCUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 6693
Db 6118 TCGTCTGCTACGTGCGAGTGAGAAATCAACAGCAATATGCGATTTCTGAAAGGAGAA 6177
QY 6694 GUUUUGCAGCAAAACGGAACAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 6753
Db 6178 GAATTTGCGTCAAAACGCGCATGGCAGTGCAGTGTATGATCAATTTGCCACCAAGAAT 6237
QY 6754 GAAGACGUUUUUUAUUAAGGAGCCUUAUGUUAAGGAGUUAUUAUUAUUAUUAUUAUUA 6813
Db 6238 GAGGACTTGTGAGTTGAAGGAGAAAGCTTGTTTAAGGAGCACCGTGATTTACAAACCGATA 6297
QY 6814 GCCAGCGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 6873
Db 6298 TCGAGCACCATTTGTCTTTGACGAATGATCTGATGGGCACACAACATCGTTGATGTT 6357
QY 6874 GUUGCUUUGGCUCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 6933
Db 6358 ATTTGATTTGTTCCCTTCATCATTAACAAAGCACTTGTTTAGAAGAAATAATAGGAACA 6417
QY 6934 UUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 6993
Db 6418 CTGTTGTTGCTCAATCACTACATGTTGTTTCAAGGTCAAGAAACACACGACTTTGCAACA 6477
QY 6994 GUUGGAGGAGGAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 7053
Db 6478 CACCTCATTTGATGGAGGACATGATTAATTTCCGATGCTTGAAGTATTTCCCACTTT 6537
QY 7054 GCACAGGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 7113
Db 6538 CTTCAAAAGCTGAAATTTAGAGAGCCAAAGGGAAGAGCGCATATGTTGTGACAAACC 6597
QY 7114 AGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 7173
Db 6598 AACTTCCAACCTAAGAGCATGCTAGCATGTTGTCAGACACTAGTTGACATTCCTTCA 6657
QY 7174 GUUGAAGGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 7233
Db 6658 TCTGATGCAATTTCTGGAAGCATTTGATTAATGCTGACTGATTTGCGGAGTCCCA 6717
QY 7234 UUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 7293
Db 6718 TTAGTATCAACTAGAGATGGGTTTCAATTTGTTGATATACACTCAGCATCGAATTTCA 6777
QY 7294 GAUCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 7353
Db 6778 ACAAAACAATTTTCAAGCGTGCAGAAACCTT---CATGGAATTTGTCACAAATCAG 6834
QY 7354 AAGGAACGAAUUGGAGCAGAAUUGGACUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 7413
Db 6835 GAGGCGAGCAGTGGTTAGTTGGGATTTAAATGCTGACTGATTTGCGGGGGG 6894
QY 7414 AUGAAACUUUACAGGUAUUGUCCCAUGCAAGAAUUAUUAUUAUUAUUAUUAUUAUUA 7473
Db 6895 CATAAAGTTTTTCATGAGCAAACTCTGAGAGCGCTTTTTCAGCCAGCTTTAAGGAACGCACTCAA 6954

Db 3027 AGCGCGCTCTTCGCTACAAATTGTTTCACGAGTGTTTATCATCGAGCCCGAGTACATGCGA 3086
QY 3611 AGAAUUCUUGUGUAAAAGCAAGAGAUUUAUUAAGGAAUGUAUUAUUAUUAUUAUUAUUAUUA 3670
Db 3087 AGAGCATTCGCGATGCGAGGCGTGCCTAAATCAATGAGGCTCTCGTCCGAACTTGTGAAAT 3146
QY 3671 GGAUUUCGGGCAACAUUUUCUUGUAGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUUA 3730
Db 3147 TCTTTTCTCTGTGTGTTTCAAAATTTTTCGCGGATGCTATAGCGACATAATATACCTTG 3206
QY 3731 UAAACUGCUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 3787
Db 3207 TGAACGTGTGTGTTTCTCTCTGCTGTACAAATGTCCATGTCTGTGCGCATGTGA 3266
QY 3788 UAUCGUUCGUAUGCACAUAUUAAGAGAGAGAAAGCAGGUGUAUUAUCGAGAAAGUUCUGA 3847
Db 3267 TAGCAGCAGACNAGGGAAGAAAGAGAGAGCGATGCGAAATAAAGCTGATGAATGAAATGA 3326
QY 3848 UGNAUAUUUAGUGGCCUUAUUAAGGAGCAGUAUAAGAGUAUUAUUAUUAUUAUUAUUAUUAUUA 3907
Db 3327 GGAAGTTAATGCTATATGTAACCAATTTTTCAGCAAGAAACAGGATGATGCGCCCATATACA 3386
QY 3908 AAGAAUUUAAGAGAGUAUUAUUAAGAAAGUAGACUUGAGUGUUAUUAUUAUUAUUAUUAUUAUUA 3964
Db 3387 ATGACTTCTTGACATGTGCGTAAATGTGAGACCAGATCTTGAGGAAACTCTCTGTGTACA 3446
QY 3965 AAGAAUUGCAAGAAAGUUAUUAUUAAGUUAUUAAGCGAAAGCGAAAGUUAUUAUUAUUAUUAUUA 4024
Db 3447 TGGCTGGCGTAGAAATGTTTCAACACAGCGCTAAGTCAGCGGTTCAGATTCATTAATTCGAGA 3506
QY 4025 AAUAUAAGCAUUGUUGCUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 4084
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QY 4085 UAUAUAAGCAGCUGAAACAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 4144
Db 3567 TTTTCAAGATTTGACAAACTCAAAACAGTTTTGTACGTTTGGAGGAAACGCTCCGAC 3626
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Db 3627 TTCAAGGGCTTGAAGACATTTGAAGCTTGGAGGACGATAAAGACTTCACAAATTTGATTTTG 3686
QY 4205 ACUAUAUUGUGGGGAGCAAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 4264
Db 3687 ATATTAACAGACGAGGCTCAATGCTCAACAACTTTGATGTCTTATTTGATGACTGCT 3746
QY 4265 GGGAAAAACAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 4324
Db 3747 GGAATCGGCAACTACAGCAAAATCGCACAGTTCACATTTACAGGACCAAGCAAAATTC 3806
QY 4325 UUGAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 4384
Db 3807 TTGAATTTACAGAAATACATGACGCTTTTGTGCGCAATGAATAGCATCATCAAGTGAAGG 3866
QY 4385 AAGAAUGGAUAGUCGUG 4444
Db 3867 GAGAGTCTTAGTAGAGGACGATAGGTTCGGAATAATCAACGAGCTTACCTGTCACATC 3926
QY 4445 UAUAUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 4504
Db 3927 TTGCCAAGAAGGTAGGTGTACTACTCGAACCTTACACGCCCTTTTGGCGGAGATGTTA 3986
QY 4505 CAGCAGUUGAGACAACAUUCCUUUUUUGCAAAACCCCAUUAUUAUUAUUAUUAUUAUUAUUAUUA 4564
Db 3987 GTAGACAGTTAGCAGGTGATCTCTTTCTTTCAAAACGTTTACATCAAAATGAGAGGGTTAA 4046
QY 4565 CAUUA 4624
Db 4047 GTTGTGTTTTCAGCAATATATACAGTATGACGAGTGGAATGCTTTTCTACTACTATG 4106
QY 4625 CAAUAUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 4684

Db 4107 TTAACAATCCATCAATTTGATGGAATTTGACTTTGTTCATCATAGACGAGTCCCATGTCA 4166
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Db 4167 CAGACAGTGGCAGCAATAGCTTTCAATTTGTGCACTTTAAAGAGTACAACTTTGTGTCGAAT 4226
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QY 5045 AACAUAUUA 5104
Db 4527 CCCATTTTCATAGTAGTACAAACATCATCGAAGATGGAAGTGCAGCTTGGATGTTGAGTGTG 4586
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Db 4587 TGTGTTGATTTTGGACTAAAGTGTGTCGAGAACTCGACAGCGAAATTCGTTGTGTCGCT 4646
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Db 4887 ACTTTGAGTAACTCTCTTCTTCCACTTATTAATCCGTCATGATGATGATGATGATGATGATGATGAT 4946
QY 5465 CUGAAUUA 5524
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QY 5525 CCAUGGCUUA 5584
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QY 5705 UUGUUA 5764
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D5 6324 TAAACGAATCTCTGATGGCTTCAAGGAGACCATGTATGTTATTTGGCTTATGGCGCAATAA 6383
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D5 6384 TCATCACTAATGACACCTCTTCAGGAACAAATGGCACACTTCTAGTCAAGTCTTGGC 6443
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D5 6444 ATGGTGAATTCATTTGTTAAATAATACCAACGCTCAAAGTGCATTTTCATAGAAGGAAG 6503
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D5 6564 GGGCAACAAACCGGAGGAACGACGATGCTTGGTTGGGCAAACTTTCAAGAAAGAGTC 6623
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D5 6624 TTCCGCTCCACTGTTTCGGAATCTTCATGACAAATACCTGAAGGAACCTGCTCATATTGA 6683
QY 7193 AAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 7252
D5 6684 TACATTTGGATTTTCGCAACGAAGGAGTTGCGGATTTGCCATGTTTCAACAACGAGAT 6743
QY 7253 GAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 7312
D5 6744 GCAAGATTAATGGAGTTTATGTTTGGCTTCCACAGTCTCATCTAAGAAATTTATTTGTCC 6803
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D5 6864 AGCATTTGGCTATGGCAACCTTAGCAAAATTTGCGTGGGGAACGCTCAACTAGTTGTAAC 6923
QY 7433 CUCAUGCAAAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 7492
D5 6924 AACAGGCGCCGAAATTTGTTATCTCAATCTAGTCAAGATTTTATCTCTGTTGTTG 6983
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D5 7101 TCTTCGAGAAATTTTACAAACAGCGAAGAGCGGCTTATTTTCAGACCCCTTAATGG 7160
QY 7673 GUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 7732
D5 7161 GAGAGTACCGCGAGCAAGTTTGAACAAAGAGCTTTTAAAGGATTTCTTTTAAATACA 7220
QY 7733 CAUAGAAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 7792
D5 7221 ATAAACCCGCTACTGTTAAACCAACTGATGATTAATTTTGGAGAGCGGATGGGG 7280
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D5 7281 TTATACGATGATGTTGATTTTGAAGTTCACGAATGTCGATTCATACAGATCCGAGG 7340
QY 7853 AGAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 7912
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QY 7913 AGCGGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 7972

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| Db | 7401 | AAGAGTATTTTGAGGGCTAGATGATTTTGTATCGAGCGCACTTTTATTCCAAAGTTGTG | 7460 |
| Qy | 7973 | UCCGAUUAUUCACGGGUAUUGUGGAUUAUGGAUGGAAGUCUUAUAAGCUGAAUUAAGAC | 8032 |
| Db | 7461 | AAAGGTTTGTTCATATGGCTACAAGAGTCTGTGGAATGGATCTTTAAAGCCGAGCTCAGGC | 7520 |
| Qy | 8033 | CAAUUGAAAAAGGUUGAAGCAAAACAAAACGGCGAACAUUCACAGCAGCUCCAAUUGAAACUU | 8092 |
| Db | 7521 | CGCTTGAGAAAGTCAGGCTTAACAAACAAGACCTTTACAGCAGCGCCAAATGTGATACAT | 7580 |
| Qy | 8093 | UACUUGCGGAAAGUUUGCGUCUGAUAUUUCAAACCAAUUUUUAUGAUCUUUAUAUGA | 8152 |
| Db | 7581 | TGCTTGGAGCTAAAGTTTGTGTGATGATTTCAACATAGTTTCTACAGGAAAAACCTCA | 7640 |
| Qy | 8153 | AAUUGCCCAUGGACUGCGGGAUGACUAAGUUUAUUCGGAUGGGAUUCUUCUAGGUA | 8212 |
| Db | 7641 | AGTGTCCATGGACGGTCGGCATGACAAAATTTATTTGGTGTGGATTAATAATGATGAGAT | 7700 |
| Qy | 8213 | AAUUCUGAUGGUUGUAUAUACCGCGAUGCUGACGGAUACAGAUUUGACAGUUUCUUA | 8272 |
| Db | 7701 | CATTACCTGATGGTTGTTGTTATGTCTATGCTGATGATGCATCACAGTTCGATGTTTCTTAA | 7760 |
| Qy | 8273 | CACAAUACUUGCUGAAUUGCAGUGUCUGGGAUUUGGGAGUUUUUAUGAAGAAUUGGACA | 8332 |
| Db | 7761 | CCCAGCCTTACTGAAACGCAAGTCTCATAAATCAGGTCATTTTATATGAGAGATTGTTGGG | 7820 |
| Qy | 8333 | UAGCGUGCAGATGUCUUUGAAAAUUGCAGUCAGAAUUAUUAACCCCCCAUUGCAACAC | 8392 |
| Db | 7821 | TCGGCCAAAGAGATGCTTGAATAATCTTTATGCCGAGATTGTGTACATCTCCAAATCTTTGCTC | 7880 |
| Qy | 8393 | CUGAUGGAAACAGUCUCUAAAAAGUUUCGAGGAUUAUAGUGGUCACACCGUACAACAGUCG | 8452 |
| Db | 7881 | CTGATGGAACAAATTTCAAGAAATTTAGAGGTAAACACAGTGGGCAACCTCTCAACAGTGG | 7940 |
| Qy | 8453 | UAGAAUACA CAUUGAUGGUCUUAUUUGUGUGCAGUAUAGUUUAUUAUGAAUAGUGUAA | 8512 |
| Db | 7941 | TGGATAACA CA TAATGTTGTGTATCTCTATTACTATGCTGTCATGAAATTTGGTTGGA | 8000 |
| Qy | 8513 | AGUUUGAAGAACGAGUAUGUCUGCAGGUUAUUUGUUAACGUGAUGAUUAUUGCUUG | 8572 |
| Db | 8001 | ACTGCGAGGAGATTGAGATAAAACTTGTCTTCTTTCGAAATGGAGATGATCTGATACTTG | 8060 |
| Qy | 8573 | CAAUCAAUCAAAAUUAUACAUAUCUAGUAUUCUUUAAAGUUAUUGCUAAUUUAG | 8632 |
| Db | 8061 | CAGTCAAGATGAGGATAGCGGCTTACTTGATAACATGTCTCTCTTTTGGCACTTG | 8120 |
| Qy | 8633 | GUUUGACUA CGAUUUCUUCUACGAAACGAAAGACAAAGGAGAA CUUUGUUUAUGUCUC | 8692 |
| Db | 8121 | GACTGAATTTATGATTTTTTCAGAACGTACGCATAAAAGAGAAGATCTTTGGTTCATGTCCC | 8180 |
| Qy | 8693 | ACAAGGAGUUAAUUAUUGACUAUGUAUUAUCCAAAGCUGGAGCCAGAGAGGGUUGUCU | 8752 |
| Db | 8181 | ACCAAGCAATGCTAGTTTGGATGTGATGTGACTCCAAAACCTCGAAGAAAGAGAGAATTTGTT | 8240 |
| Qy | 8753 | CAAUACUUGAGUGGGAUAGAGUAAAAACAGAAACACAGAUUAGAGCAUUGCGCUU | 8812 |
| Db | 8241 | CAATCTTAGAGTGGGATAGAAGCAAGAAATTTAGCACCGAAACAGAGGCTATTTTGGCTG | 8300 |
| Qy | 8813 | CGAUGAUUGAAGCAGUGGGUUUACCUUAGGUUUAUCCACGAAAUUCGAAAAUUUUUGCUU | 8872 |
| Db | 8301 | CGATGATTGAGGCATGGGGGCACACCCAGCTCTTGCAAGAAATTCAGAAAGTTTTCACCTAT | 8360 |
| Qy | 8873 | GGGUUCUGGAACAGACCAUACAAUACUUCGCAUCUGAGGGAAGGCAACCAUACAUU | 8932 |
| Db | 8361 | GGTTCGTTGAAAAGAAAGAGGTGCGAANTTGGCAGCCCTCGGAAAAGCTCCATACATAG | 8420 |
| Qy | 8933 | CGGAAACAGCGCUCAAAAGACUUUAACAUCUGCGAAGAAAGGAUGUGUGAUGAAAUCAUGU | 8992 |
| Db | 8421 | CTGAGACAGCACTTCGTTAGTTTATACACTGCAAGGGAGCAGATACAAGTGAACCTGGCAC | 8480 |
| Qy | 8993 | CAUA CUUAGAGUUGUGCAAGUUAUUGAACGAGAGUAGUAUCUUUGAUGAUGAAGAUG | 9052 |

| | | | |
|----|------|--|------|
| Db | 8481 | GCTACCTACAA-----GCCCTCATCAAGATATCTTCTTTGTGCAAGGAGA-- | 8526 |
| Qy | 9053 | UUUCUACCAGUCGCUUGAUGCUGGCAAAACCCACAGCAGAAAAACAAGAAAGACGAUG | 9112 |
| Db | 8527 | -----CACTGTGATGCTCAATCAGGCATCAGCCAACTGTGGCAGATGCTG | 8573 |
| Qy | 9113 | AAGAGAGAAAGAAUAAAGAAAGAAAGCAGGAAAUAAAAACAAGAAUAAAGAGUCGAGA | 9172 |
| Db | 8574 | GAGCTACAAAGAAAGATAAAGAAAGATGACAAAGCGGAAAAACAAGGAGCTTACAGGCTCCG | 8633 |
| Qy | 9173 | AGAAAUAUGAGAAAAUUUCGAAUAGCCAUUCUGGUGCUUUGUUUUAACAACAACGAAAAAG | 9232 |
| Db | 8634 | GCTCAGGTGAGAAA-----AGTAGCAGCTGTCTACGAAGG | 8669 |
| Qy | 9233 | ACAAGGAUGCUGAUGAAGGAUAGUGAUCUUUCAUACACGACGAUUAUAAUCGAUU | 9292 |
| Db | 8670 | ACAAGGATGGAATGCTGGTCTCATGGGAAA---ATTGTCCGCGTCTTTCGAAGATCA | 8726 |
| Qy | 9293 | CCAAUAAACUCACAAUUGCCAAAAAGUAGAAAGGAAAGAAUUUAAAAUUUGGAGUCCUUU | 9352 |
| Db | 8727 | CAAGAAAAATGCTCAATGCCACGCGTGAAGGAAATGTGATACTCGATATTGATCATTTGC | 8786 |
| Qy | 9353 | UACAAUACACACAGAUCAAGUGACAUUUCAAUACACAGGCGCAAGUAUUUUCACAGUUUA | 9412 |
| Db | 8787 | TGGAAATATAACCGGATCAAATTTGAGTTATATAACAACACGAGCGTCTCATCAGCAGTTG | 8846 |
| Qy | 9413 | AUACAUGUAACAACGUCUGAAGAAUCCUAUGUGUGUCUGAUGAAGAAUUGGGAUAA | 9472 |
| Db | 8847 | CCTCTTGTTCAACCAGGTTAAGACGGAATATGATTTGAACGAGCAACAGATGGAGTTG | 8906 |
| Qy | 9473 | UUUGAAUGAUAAUUGUUUGUGUAUUGAAAAUGGAAACAUUCCAAAUAUAAUUGGCA | 9532 |
| Db | 8907 | TAATGAATGTTTCATGTTTGGTGATTCAGAAATGSCACTTCACCCGACATTAAATGGAG | 8966 |
| Qy | 9533 | UGUGUUUAUGAUGCAAGGGGAAGAACAAAUUCGAUACCCCUUACACCAAUAGUGAAAA | 9592 |
| Db | 8967 | TGTGGGTTATGTGACGACGAAATGACAAAGTTGAGTATCCCTTGAAACCAATATGTTAAA | 9026 |
| Qy | 9593 | ACGCAAAACCCAUUUGCGUCAGUAUUGCUCAUUUAAGCAUUGUUGCUGAAGCAUCA | 9652 |
| Db | 9027 | ATGCAAAAGCCAAACGCTCGGCAAAATAATGCATATTTTCAGATGACGCGGAGCATATA | 9086 |
| Qy | 9653 | UCGAAAAAGAAAUAUUGAAGACCAUAUUGCCGAGUACGGUUAUUAACAGGAACCUCA | 9712 |
| Db | 9087 | TAGAGATGAGAAATGACAGAGCCACCATACATCGCAGGTATGTTGCTTCGAAACCTAC | 9146 |
| Qy | 9713 | CCGCAUGAUUUUGCCGCAUUGCUUUUUAUUGAAUUAUGAACAUCAACGAAGGACGCCAG | 9772 |
| Db | 9147 | GGGATAGAGTTTAGCAGCATATGCTTTTCATTTCTATGAAGTCAATTCCTAAAACTCCTG | 9206 |
| Qy | 9773 | CUCGGCCCGGAGCCCAUCCAGAGUAGAACUCGACGCAUUGCCGAGUUGCGAAUAAUA | 9832 |
| Db | 9207 | AAAGAGCCCGAGAGCTGTTGGCGCAGATGAAGACGACGCTCTTAGCAATGTTTCTTCAA | 9266 |
| Qy | 9833 | AGAUUUUGCAGUGAUGAAAAAGUCGGAUUGCCAGUCUGAGAACACGGAGCGCCACACCG | 9892 |
| Db | 9267 | GTTTGTGTCCTTGATGGAATGTTGCCACCATAGCAGGAAGACATCTGAACGGCACACTG | 9326 |
| Qy | 9893 | CAGACGAUUUAAACCAUAAACAUCAUCGAUUAUCCCGCGU | 9932 |
| Db | 9327 | CACGTGATGTTAATAGAAACATGCACACCTTACTTAGGTG | 9366 |

RESULT 8

RESOPI 0
AAT47073

ID AAT47073 standard; RNA; 8543 BP.

XX

AC AAT47073;

XX

DT 17-OCT-2003 (revised)

DT

XX
DE Maize dwarf mosaic virus genomic RNA.

Db 5497 GCAACAUAUUGUCGAAUUAUAGUCUUGCAUACAAGAGUGAAACACUAUAUUCUUUG 5556
QY 7310 CGAAUUUGACAGCGGUUUGAAGGCGAUUAUAUAUAAACAGUUGAAGGAACUGAAUUGGG 7369
Db 5557 UCGGUGGUCUGAGAACTUUAAUUGAAUAUCAUAAUGGACUCUGCAAGCAAAUAAUUGGG 5616
QY 7370 AGCAGAAUUGGACUAACAGUUAUAUCUGUUAUUGGGGCAACAUGAAACUUCAGGAUA 7429
Db 5617 AAAAAAGGAGGACUAUAAUCCGAAUUCUCAUCCUGGUGUGACUAAAUUAGUUGAUU 5676
QY 7430 GUGGUCUUGCAAGAAAUUCAAACAAUAAGUUGAUAGCGACUUAUUGCAGCGAACCTUG 7489
Db 5677 CAGCCCAAAAGGUUUGUUAUAAACGUAUUGUAGAAAGACUUGGACGCGGCGUUG 5736
QY 7490 UGUGGCGUCAGAGUAGCAUAAGUUGAUGUUAUAUAUACGCUUGAAGGAAAUUUGA 7549
Db 5737 A--AGAGCAUUGCAAGAUCAACCGAAACAUGGUCACAGAGCAAUUACAAGAAUAUUUAC 5793
QY 7550 AAGCGGUCGAUAUUCCAAUAACUUUGUUAACAAGCACAUUGUGAAGAGCAAGUA 7609
Db 5794 AAGUGGUUGCGAAAUUGUCCAGGCGCAACUAGUUUACCAAGCAUGUGUUUAAAGGUGUCAAUGCC 5853
QY 7610 AAUUGUUUAAUUGUAUCUGCAAAACUGUAGUGAAGCGAAUGAGUUCUUUAAACCAACUGA 7669
Db 5854 CACAUUUCAAUUGUAUUAUACACACAGUACGAUGCUUUAAGAAUAUUAUUCGCCACCAUGC 5913
QY 7670 UGGGUUUUAUUGGGAAGAGCGGUUCUCAAACAGGAAGCAUAUAUAGGACCUUAUUAAU 7729
Db 5914 UUGGAAAAUACACAGAGAGUAGGCUUUAACAGAGCAGCUUUUAUCAAAGACAUAUCAAUAU 5973
QY 7730 ACUCAACGAAUAUCAAUUGGGAAGGUGCGACACUGAGAGAUUUGAAGUAGCAGUUGGGC 7789
Db 5974 AUGCAAAACCAUUAUACAUUGGAGAAUUCGUAUGAUUUUUGAUAGGCGUGUACAGC 6033
QY 7790 AAGUCAUCGAAAUUAUUGAUGCAUUGAAACUUUAGGGAUUGCAAGAAUAUUAACCGAUUGUG 7849
Db 6034 GGGUUGCAAAUUAUUCUCAAUAAUUGUUGAAUGCAACAAGUUGUUAUUAUGUCAAGAGAG 6093
QY 7850 ACCAGAUUUUGAAUUAUUGAAACAUUAAAGCGGCGAGUCGGGCGUUGUAACAGUGGUAAGA 7909
Db 6094 AAGAAAUUUUCAGAUACAUUAAACCUAGACGCGAGCUGUCGAGCAUUGUAUAACAGGAAAGA 6153
QY 7910 AAAGCGUAUUCUUGAAAUUCCAUUUAUGAUGCAUGAAUUAUUGCUUAACAGCUUAGUU 7969
Db 6154 AGAAAAUUUAUUUGAAAAUUUUUUAAGCGAAGACAAAGAAAUUCGUGAUGAGAUCCU 6213
QY 7970 GUCUCGUAUUUUAAGGGUGAUUUUGGAAUUUUGAAUUGGAAAGUCUUAAGCUGAAUUA 8029
Db 6214 GUGAAGCUUAUUAACAUGGSCAACTUUGGCGUAUGGAAUGGAUUGCAAGCUGAGAUCA 6273
QY 8030 GACCAAUUGAAAGGUUGAAGCAAAACAAACCGCAACAUUCAAGCAGCUCUCAAUUGAAA 8089
Db 6274 GACCAUAUAGAGAAACCAUGCUGAAUAAGACUCGAAACCUUCAAGCGGCCCCCAUUGAAA 6333
QY 8090 CUUUAUUGGCGGAAGGUUUGGUCGUAUUAUUAACAACCAUUAUUAUGAUUAUA 8149
Db 6334 CUUUGCUGGAGGAAAGUGGUGGUGGAGUAUUUUAUAAUCAAUCUUAUUCACAUAU 6393
QY 8150 UGAAAUUGCCUUGGACAGUCGGGAGUACUAAAGUUUUUUGCGGAUGGAUGAUUUUCUAG 8209
Db 6394 UAGAAGUCCAUUGGACUUGUUGGGAUAAACAAAUUCUUAUGAGGUUGAAUCCUUAUUGG 6453
QY 8210 GUAAACUUCUGAUGUUGGAUUAUACCGCGAUGCUGACGGAUCAAGUUUGACAGUUCUC 8269
Db 6454 AGAAGUUAACGAAGAGGUGGUUUAUCUGCGAUGCUGACGCGGUCUCAAUUUGAUAGUUCGU 6513
QY 8270 UUAACCAUAUUCUGGAUGCAGUGCTUCGGGAUAGGAGUUUUUAUGGAAGAUUGGG 8329
Db 6514 UAAACCAUAUUCUCAAUGCAGUAUUAUAAUUAUUGCAUUGCAAUUUUAUGGAAGAUUGGG 6573
QY 8330 ACAUAGGCGUGCAGAUUGCUAGAAUUUUGCACACUGAAAAUUAUUAACCCCAUUGCAA 8389

Db 6574 AUUAAGGAGCGCAAAUGCUAAAGAACCCUGUACACUGAGAUUGUUAACACCAACUGCAA 6633
QY 8330 CACCUGAUGGAACAGUCUCUCAAAGAUUUCGAGGAAUAUAUAGUGUCAAACGCUAACAG 8449
Db 6634 CGCCAGACGGAUCAUUCGUGAAGAAAUUCAAGGUAACAUAAGCGGACAACCCUUCUACAG 6693
QY 8450 UCGUAGUAUAAACAUUAGUUGUCUGUAUUUUGUGUCAGUAUAGUUAUUAUUAUGAAUAGUG 8509
Db 6694 UAGUGACACAACAUAUGAUGGUUAUAUAGCUUUAACAUAUGCCAUGCUUAACAUGGUUA 6753
QY 8510 UAAAUUUUGAGAAUCAGGAUGAUGUCGAGGUAUUUCGUUAAACGGUGAUAUUUAUUGC 8569
Db 6754 UCAAGAAAGAAAUUCCAUAAUUGCUCUGAGAAUUGUCGGAUUGGUGAUGACUACUCC 6813
QY 8570 UUGCAAUACAUAUCCAAAAUUUAUAACAUCUUAUAUUUUUAAGUUAUUAUUGCUAAU 8629
Db 6814 UAGCAGUGCAUCCUGAUUUUUGAGUUCAUUUUAUGAAUAUUUCAAUUAUUAUUGGGAUC 6873
QY 8630 UAGGUUUAAGACUACGAUUUCUCAUCGAAACGAAAGACAAAGGAGAACTUUGGUUUUAUG 8689
Db 6874 UUGGCGUAAACUUCCGAUUUAUCAACGAAACAGGAAUAUAUCCGAAUCUGUGGUUCAUG 6933
QY 8690 CUCACAAAGGAGUUAUUAAUUGAUAUUAUCCAAAGCUGGAGCCAGAGAGGUG 8749
Db 6934 CCACAAGAGGCAUCAAGUAUGAAGGAUUUAUAUACCAACCAAGCTUGAGAAAGAAUAUAG 6993
QY 8750 UCUCAAUAUUAUUGGUGGUAUAGAGUUAUAAACAGAAACAGAUUAAGAGCAUUGCG 8809
Db 6994 UGCCAUUAUUGGAGUUGCAUCAAACUUGCCUGAAUAUAGGUUGGAGCUUAUUGUG 7053
QY 8810 CUUCCGAUAUUGAAGCAUUGGUGUUAUCCUAGGUUAUUAUCCAGAAUUAUUGAAUUUAUUG 8869
Db 7054 CAGCGAUGUUGAGCCUGGGGAUAUUAUCCGAUCUUGUUAUGAAUAUAGAAUUAUUAUG 7113
QY 8870 CUUGGUCUUGGAAACAGCAACCAUAUUAUUAUUCGCAUUCUGAGGGAAGGCAACAUA 8929
Db 7114 CGUGGUUUUGGAAUUGCAACCUUUUGCAAUUCGCAAAANAAGGUGUGGCCCAUAUA 7173
QY 8930 UUUUGGAAACAGCGCUCAAAGACUUUAACAUGCGAAAGAGGAAGUCUGAUGAAUA 8989
Db 7174 UUGCGGACAGACACUCCGCAUUCUUAUUCUUGGAAACGGGUUAUCAAAGAGGAAGAAUUG 7233
QY 8990 UGUCAUAUUAAGAGAUUGUGCAAGUGAUUUGAAGCAGAGUAGUAUUUUGAUGAUGAAG 9049
Db 7234 AAAAAUUAUUAACAUAUUAAGAUUUAUUAUGGUAUUAUUAUUAUUAUUAUUAUUA 7293
QY 9050 AUGUUUUCACAGUCCGCUUUGAUGCUG-----GCAAAACCCACAGCAAGAAACAG 9102
Db 7294 AUGUAUCCAUCAUGCGGAACTUGUUAUGCGGUGCAACAGCGCGCAGUGGAAGCCAAG 7353
QY 9103 AAAGACGAUAGAGAGAAAGAAUAUAAAGAAAGAGGAAAUUAUAAACAAAUAA 9162
Db 7354 GGACAAACCAACCAAGCAACAGGUAUGGAGCAAAACAGGCCACCUCAAGGGCAGAUUUG 7413
QY 9163 GAAUUCGAGAAAGAAC----- 9178
Db 7414 GUAGUACACAGGAGCUGGAACUGGUGUAUUAUGGAAGUUAAGCAGCAGUGGCA 7473
QY 9179 -----AUGAGAAA 9187
Db 7474 CUGGACGGGAUUGGAGCAACCGGAGGCAUAUAGGAUUCUGGAAGUGGCAUGAACAGG 7533
QY 9188 CUUUGAAUAGCGCAUCUGUGCUUAUUGUUAUUAACAACGAAAGACAGAGGAGUGGUG 9247
Db 7534 UUAACACGGGUUACAGCAGAAAUUAUUGCAAUCUGGAGGCCAAAGAGAUAGGGAUG 7593
QY 9248 UAGGAUAGUGGAUUCUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 9307
Db 7594 CAGGCUUAACAGGAAAAUUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 7653
QY 9308 UGCCAAAAUGAGAAAGGAAAGAAUUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 9367
Db 7654 UACCUAAAGCAAAAGGAAAAAGAUUGGUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 7713

Db 781 CATGTGTTATGATCAAGGGAGAGACAAATCGAATACCCCTTCAACCAATAGTGA 840
QY 9591 AAACGCAAAACCCACUUUGGCGUCAGAUUAUGGCUCAUUUAGCAUUUGUUGUGAAGCAUA 9650
Db 841 AAACGCAAAACCCACTTGGCTCAGATTATGGCTCACTTTAGCAATGTTGCTGAAGCATA 900
QY 9651 CAUCGAAAGAGAAUUAUGAGAGAGCAUAUUGCCGAGGUAGCGGUUAUCAAGGACCU 9710
Db 901 CATCGAAAAGAGAAATTTATGAGAAGCCATATATGCGGAGGTACGGTATTTCACGGAACCT 960
QY 9711 CACCGCAUGAGUUGGCGGCAUUCUUUUGAUUUUUAUGAAUUGACAUCAAGACGCC 9770
Db 961 CACCGACATGAGTTTGGCGGATATGCTTTGATTTCTATGAAATGACATCAAGACGCC 1020
QY 9771 AGCUCGGGCCGGGAAGCCCAUCCAGAGAAAGCUGCAGCAUUGCGAGAUUGCGAAUA 9830
Db 1021 AGCTCGGGCCGGGAAGCCCAATCCAGATGAAAGCTGCAGCATTCGAGATGCGAATAA 1080
QY 9831 UAGAUGUUUGNCUGAGUGGAAAGUCCGAAUUGCGAUGGACGACACGAGGCGGCACAC 9890
Db 1081 TAAGATGTTTGGACTGGATGGAAGATCGGAATGCGACTGAGAACACGAGGCGGCACAC 1140
QY 9891 CGCAGACGAGUUUAACCAUAACACUACUACUACCGCGGUUCGAAUUAUUAUUAUUA 9950
Db 1141 CGCAGACGATGTTAACCATAACTCATGATTCACCGGCTTCGATATTATAGATATT 1200
QY 9951 UACCUAAGCAUAGUUUAUCUAGAUUUUUUUAUUAUUGCGAUUAGCUUUUACGACG 10010
Db 1201 TACCTAAGCATAGTTTATCTAGTATCTTTTAAATCGCATTTACTTTACTTCTAGCAG 1260
QY 10011 CGUUGAGGAGUUUAUCCUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 10070
Db 1261 CGTTAGTAGGTTTACCTTCTATTATCTATGTTGTCAGTGAGGTTAGCCCTCGTGTGATC 1320
QY 10071 UCUTUAGAAUUAUUGCCCAAGCUGCAGUGGCGUUGUUAUUAUUAUUAUUAUUAUUAUUA 10130
Db 1321 TCTTAGAAGTATTGTCACAGCTGAGTGGCTGTTGTTTCATAGCATGATGGCTCATG 1380
QY 10131 GACCUUACGCUAAGCAAGAGGG 10154
Db 1381 GACCTTCAGCTTAAGCAAGAGGG 1404

RESULT 10
AAT64457
ID AAT64457 standard; RNA; 1404 BP.

XX AC AAT64457;
XX 27-AUG-2003 (revised)
DT 02-JUN-1997 (first entry)

DE Coat protein gene RNA from PLDMV.
XX Papaya malformed leaf mosaic virus; PLDMV; coat protein gene;
KW transgenic plant; resistant; ss.

XX Papaya leaf-distortion mosaic potyvirus.
OS
XX Key Location/Qualifiers
FH 2..1195
CDS /*tag= a
FT /product= "PLDMV coat protein"

XX JP08322572-A.
PN
PD 10-DEC-1996.
XX
PF 24-MAR-1995; 95JP-00066501.
XX
PR 24-MAR-1995; 95JP-00066501.
XX

PA (NORQ) NORINSUISANSHO KOKUSAI NORIN SUISANGYO.
XX WPI; 1997-081086/08.
DR P-PSDB; AAW14844.
XX
PT DNA encoding papaya malformed leaf mosaic virus (PMLMV) coat protein -
PT useful for the creation of PMLMV-resistant plants.
XX
PS Claim 1; Page 4-5; 6pp; Japanese.
XX
CC The sequences given in AAT64557-58 represent the RNA and cDNA from the
CC papaya malformed leaf mosaic virus (PLDMV) coat protein gene. These
CC sequences may be used to form transgenic plants which are resistant to
CC PLDMV infection. Plants such as this are important in industry. (Updated
CC on 27-AUG-2003 to correct OS field.)
SQ Sequence 1404 BP; 475 A; 257 C; 321 G; 0 T; 351 U; 0 Other;
Query Match 13.8%; Score 1404; DB 2; Length 1404;
Best Local Similarity 100.0%; Pred. No. 4.6e-306; Mismatches 0; Indels 0; Gaps 0;
Matches 1404; Conservative 0;
QY 8751 CUCAUAUCUUGAGUGGGGAUAGAAGUGUAAAACCAAGACACACAGAUUAGGCGAUUUGCG 8810
Db 1 CUCAUAUCUUGAGUGGGGAUAGAAGUGUAAAACCAAGACACACAGAUUAGGCGAUUUGCG 60
QY 8811 UUCGAUGAUAGAAGCAUGGGGUUACCUAGGUUAUCCAGAAUUCGAAAAUUUUUUGC 8870
Db 61 UUCGAUGAUAGAAGCAUGGGGUUACCUAGGUUAUCCAGAAUUCGAAAAUUUUUUGC 120
QY 8871 UUGGCUUCUGGAAACCAAGCACCAUACAUCUCGCAUCUGAGGAGAAAGGCCACCAUACA 8930
Db 121 UUGGCUUCUGGAAACCAAGCACCAUACAUCUCGCAUCUGAGGAGAAAGGCCACCAUACA 180
QY 8931 UUCGAAAAACAGCGCUCAAAAAGA CUUUAACAUCUGGAAAGAAAGGUGUGUAUUAUUAU 8990
Db 181 UUCGAAAAACAGCGCUCAAAAAGCUUUAACAUCUGGAAAGAAAGGUGUGUAUUAUUAU 240
QY 8991 GUCAUAUCUUGAGAUUGUGUGCAAGUUAUUGAACGAGAGUAGUACUUUGAUGAUGAAGA 9050
Db 241 GUCAUAUCUUGAGAUUGUGUGCAAGUUAUUGAACGAGAGUAGUACUUUGAUGAUGAAGA 300
QY 9051 UGUUUCUCACAGUCGCGCUUUGAUGUGGCAAAACCCACAGCAGAAAAACAAGAAAGACA 9110
Db 301 UGUUUCUCACAGUCGCGCUUUGAUGUGGCAAAACCCACAGCAGAAAAACAAGAAAGACA 360
QY 9111 UGAAGAGAGAAAGAAUAAAAGAAAGAAAGCAGGAAAAUAAAAACAAGAAUUAAGAGUCCA 9170
Db 361 UGAAGAGAGAAAGAAUAAAAGAAAGAAAGCAGGAAAAUAAAAACAAGAAUUAAGAGUCCA 420
QY 9171 GAAGAAAAAUGAGAAAAACUUCGAAUAGCGCAUCUGGUGCUAUUUGUUAACAACGAAAA 9230
Db 421 GAAGAAAAAUGAGAAAAACUUCGAAUAGCGCAUCUGGUGCUAUUUGUUAACAACGAAAA 480
QY 9231 AGACAAGAGUGUGCAUGAGUAGCAUAAAGUGGCUUUAUUAUUAUUAUUAUUAUUAUUA 9290
Db 481 AGACAAGAGUGUGCAUGAGUAGCAUAAAGUGGCUUUAUUAUUAUUAUUAUUAUUAUUA 540
QY 9291 AUCCAUAUUAUCACAAUUGCCAAAGUGAGAAAGGGAAGAAAGAAUUAUUAUUAUUGGAGUUCU 9350
Db 541 AUCCAUAUUAUCACAAUUGCCAAAGUGAGAAAGGGAAGAAAGAAUUAUUAUUAUUGGAGUUCU 600
QY 9351 UUUACAUAUACACACAGAUCAUGGCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 9410
Db 601 UUUACAUAUACACACAGAUCAUGGCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 660
QY 9411 UAAUAUUGGUACACCGCUUGAGAGAAUCCUAUUGGUGUGUGUGUGUGUGUGUGUGUGUG 9470
Db 661 UAAUAUUGGUACACCGCUUGAGAGAAUCCUAUUGGUGUGUGUGUGUGUGUGUGUGUGUG 720
QY 9471 AAUUUUGAAGGAUUAUUGGUUUUGGUGUAUUGAUAUUGAUAUUGAUAUUGAUAUUGG 9530
Db 721 AAUUUUGAAGGAUUAUUGGUUUUGGUGUAUUGGUAUUGGUAUUGGUAUUGGUAUUGG 780

| | | | |
|----|------|--|------|
| Qy | 6760 | GUUUCUUUUUAAGAGGCGCUCAAAGUGUGAAAGGGAUUGCGCAUUUAACAAGUGUGUAGCCAGC | 6819 |
| Db | 421 | GTTGAGCATGAAGCCCGCTCGTTAAATAGAGGGCTCGCGATCACACCAAGTATCGAAG | 480 |
| Qy | 6820 | GCUAUUUGCCAAUCACAAAACACU-CAAUUGUGCGUCCACCAACACUUAUUGGGGUGG | 6878 |
| Db | 481 | TTGATTTCGAAGTTGGAAATGATTCGCGATGATGTGTACCTCAATTCTCATCGTGTGG | 540 |
| Qy | 6879 | CUUUGGCUCAUACAUAAGUUAUAUGGCACUUGUUUAAAGAAUAAUUGGGAUUUAUU | 6938 |
| Db | 541 | CTTCGGTCCATTATAATTACAATCGTCATTACTCAAAGGAACAATGAACCCCTTCGA | 600 |
| Qy | 6939 | GAUCAAUUGCAGCGCAUGGAAUUUAUAUCAGGAACUCCACAGCAAAUUAUAAAGUCUGCG | 6998 |
| Db | 601 | G-TCAAAACAGCACATGCGACTTCAAGTGGCTTAAACAAGAGAGATGAAGTGTTC | 659 |
| Qy | 6999 | AGUGGAGUAUGGAUAUUGCCAUUCUCAAUUGCCUAAAGACUCCACCCUUUGCACA | 7058 |
| Db | 660 | CGTAGAGAAACATGACATTCCTGCTCATAGGCTTCCAAAGATTTCCACCATTTCCAGT | 719 |
| Qy | 7059 | GAGGUUACGUAUAGAAAUCAAUAGUGGGUGAAUCAAUUUGUCUUGUUGGAAUACGUU | 7118 |
| Db | 720 | GAAGAGTAAGTTTAGAGAGCCCAAGTCAATGATTCAATTTGCTTAGTTGGCACAACTT | 779 |
| Qy | 7119 | CCAAGAAAAGUACAUGCAAGCAUCGUUUUCUGAGACAAGCAAAACAUAUCCACGAGUUGA | 7178 |
| Db | 780 | TCAAGAGAAGTTTTTGAGTAGTCTTATTTCAGCAGATAGCAACAATCACCACTGAGTGG | 839 |
| Qy | 7179 | AGGUAGUUUUGGAAACAUIUGAUUAUAACAACGGAAGGACUUGUGGAUUGCCUUUAGU | 7238 |
| Db | 840 | ATCAAAGTTTTGGAGACACTGGATGTGATCAAGAGATGGACACTGTGGCTTGGCATAGT | 899 |
| Qy | 7239 | UAGUGUCAUGAGUGGAUUUAUUGUAGGAUAACAUAUUAUAGAGUACAUAAGUACGAUCA | 7298 |
| Db | 900 | AGCTCGAGATGATGCTGCAATTTGTGGTTTCACAGTCTCACAGTATCAACACAGAACA | 959 |
| Qy | 7299 | UAUUUUUUCUGNAUUUUGAGACGCGUUUGAAGGCGAUUAUUAACAAGUUGAAGGA | 7358 |
| Db | 960 | AAACTACTTTTCAGCTCTTCAGAAAGCTTT--CATGGAAATTAATTTGCCAGGTGGAGAC | 1016 |
| Qy | 7359 | ACTUGAAUGGGAGCAGAAUUGGACUUAACAGGUUAUAUCUGUUAUUGGGGCAACAUGAA | 7418 |
| Db | 1017 | TTTAGATGGCGGAAAGATTTGGGTGTACAATCCAAATGAAATAGGATGGGGCTCTTGAA | 1076 |
| Qy | 7419 | ACUUCAGGAUAGUCUCCAUUGCAAGAAAUUCAAACAACAAUAGUUAUAGCGACUUAUG | 7478 |
| Db | 1077 | ATTGAAGAGCGATCAACCGACTGGAATGTTTAAGATTTGAAAACTCATTGAGGATATCCA | 1136 |
| Qy | 7479 | CACGGAACUUGUGCGCUCAGAGUACCAUACAUGUUAUGUUAUUAUAUACAGCUUGA | 7538 |
| Db | 1137 | GTCAGCATTTGTTTCGTGAGCAAGCAAGTGATA-----ATGGCTGTATGCACAGTTTCA | 1190 |
| Qy | 7539 | AGGAAAUUUGAAAGCGUUGCAUAUUCCAAUAUCUUGUUAACAAGCACAUUGUGAA | 7598 |
| Db | 1191 | AGGGTTCTTCAAGCCGTGCCAAGATGAGAGCCAACTTTGTACCAGCACATTTGTTAA | 1250 |
| Qy | 7599 | AGGACGAUGAAAUUUGUUAUUGUAAUCUGCAAAUCUCUAGUGAAGCGAAUGAUUCUU | 7658 |
| Db | 1251 | GGGACCATGCCGTTGTTTCATCTTTATCTCAGCACACATCGTGAGCGCAAGACAAATTTT | 1310 |
| Qy | 7659 | UAAACCAUGAGUGGUUUUAUGGGAAGAGGGGUUCUACAACAGGAAGCAUAUAUAAAGGA | 7718 |
| Db | 1311 | CCAAACCCCTTCATGGGTGCGTATGGTATAGACCGGATTAATTCGTAATTCCTTATGCTAAGGA | 1370 |
| Qy | 7719 | CCUUAUUAAUAUCUACAGAAAUAACCAUUGGGGAGGUCGACACUAGAGAGAUUUGAAGA | 7778 |
| Db | 1371 | CATTTTCGAGTATTCACACTGAAATAGAAAGTTGGGAAGGTTGATACATGTGCACTTGA | 1430 |
| Qy | 7779 | UGCAGUUGGGCAGUACUCCGAAAUUAUUGAUGCAAUUGAAAUUUGGGGAAUUGCAAGUUAU | 7838 |
| Db | 1431 | GCCCGTTTGAAGCAGCGTAATTGAGACTTGCATGCTGTCAAAATGATATCTTGCATATG | 1490 |

| | | | |
|----|------|--|------|
| Qy | 7839 | CACCGAUGUGACCGAGUACUUUGAAUCAUAUGCAAGAAGCGGACUGUCGGUGCUUGUA | 7899 |
| Db | 1491 | CACTGATGAAGAAGAGATTTTCCAAATCTCTTAACATGAAGAAGCAGCTGTGTGGTGCAATTGA | 1550 |
| Qy | 7899 | CAGUGGUAGAAAAGCGUACUUCGAAAAAUCCACAUIUGAUGUCGAAAUACAUIUGCU | 7958 |
| Db | 1551 | TAGGGTGAAGAACCGGAGTATTTTGAACATACACCCAAGGACAAAGAGCGAATACT | 1610 |
| Qy | 7959 | ACAGCUVAGUUGUCUCCGUAUUAUUCAAAGGGUGAUUUGGGAAUUTUGGAUUGGAAGUCUUA | 8018 |
| Db | 1611 | GTTTGAAAGTGTCTTAGACTGTATAAAGGAAACCTTGGAGTGTGGAATGGTTCAATCAA | 1670 |
| Qy | 8019 | AGCUGAAUUAAGACCAAUUGAAAAAGGUAGCAAAACAAACCGGACAUUCACACGACGC | 8078 |
| Db | 1671 | GGCTGAGCTTAGACCTATTGAGAAAGTCGTGTAAACAAGACGCCGAACCTTTTACGACGC | 1730 |
| Qy | 8079 | UCCAAUUGAAACUUACAUIUGCGGAAAGUUCUGUCUGAUUAUCCAAACCAAUUUA | 8138 |
| Db | 1731 | ACCATTGGATACGCTACTAGCTGGCAAGTTTCGTTTGATGATTTCAACACCAGTTCTA | 1790 |
| Qy | 8139 | UGAUCUUUAUAGAAAUUGCCCAUGGCAGUCGGGAUGACAUAAGUUUAUUGCGGAUGGAA | 8198 |
| Db | 1791 | CTCAAGCACACACTTCGCACCATGGAGTGTCCGAATTTCAAATAATCTCGSGTGTGGGA | 1850 |
| Qy | 8199 | UGAUCUUUAGGUAAACUUCUCUGAUGUUGGAUAUACCGGAUGUCUGACGGAUCAUAU | 8258 |
| Db | 1851 | TAGATTTTGGAGAAACTTACTACGGATGGATATACTGTAGGCGAGATGGCAGTAGATT | 1910 |
| Qy | 8259 | UGACAGUUCUUAACCAUAUUGUGAUGCAGUGUCGCGGAUAUUGGGAGUUUUCAU | 8318 |
| Db | 1911 | TGATAGTTCCTTAACACCATATCTCAATAATGCTGTGGCGTCCATCCGCTGGAATTCAT | 1970 |
| Qy | 8319 | GGAAGAUUGGGA CANAAGGCGUGCAGAGUC---UUCGAAAAUUGCACACUGAAAAUUA | 8375 |
| Db | 1971 | GEAACCTGGGGAATCGGGAGCAATGCTTAATGAGGAACCTGTATGCCGAATCATATA | 2030 |
| Qy | 8376 | CACCCC AUUGCAACACCUAGUGAAACAGUCUCUAAAAAGUUUCGAGGAAUUAUAGUGG | 8435 |
| Db | 2031 | TACTCCCATTTCTCACTGCTGATGGAACGATAGTTAAGAAAGTCCAAAAGGCAATAACTCGGG | 2090 |
| Qy | 8436 | UCAACCGUACAACAGUCUAGUAUAACHACUAUGAUGGUCUGUAUUUGUGCAGUAUAGUU | 8495 |
| Db | 2091 | ACAACCATGCACAGTCGTGGATAACACACTCATGTGGTGTAGTGGCAATGAAGTACTCACT | 2150 |
| Qy | 8496 | AUUUAUAUAGUGUUAAGUUUCAGAAUACAGGAUGAUGUCUGCAGGUYAUUUCUUUAACGG | 8555 |
| Db | 2151 | ACGTGCTCGGTATTTATATAGGATCAAAAACGACGAGGGCGTTTTCTTTGCCAATGG | 2210 |
| Qy | 8556 | UGAUAUUUAUUGCUUGCAAUCAUAAUUAUUAACAUCUCCUAGAUUUUUUUAAGU | 8615 |
| Db | 2211 | TGATGACTTTAATTGTCTCAGTTCCGCCAAGTGATGAATGGATTTTGCACTCGTTGCAGGA | 2270 |
| Qy | 8616 | UCAUUUGCUAUAUUAGGUUUAAGUACUACGUAUUCUCUACUGAACGAAGACAAAGGAGA | 8675 |
| Db | 2271 | CCGTTCTTCAGAGCTAGGCTTGT CATATGATGTTTTAATGAACGAAACACAGATAGATCAGA | 2330 |
| Qy | 8676 | ACTUUGSUUAUUGUCUACAAAAGGUAUUAUUAUGACUAUCUAUUAUCCAAAGCUGGA | 8735 |
| Db | 2331 | GCITTTGGTTTATGTCCCATCAAGAAATTTTAAATTGAGAAATCAATATATCCAAAGCTTGA | 2390 |
| Qy | 8736 | GCCAGAGAGGUUGUCUCAAUAUCUGAGUGGGUAGAGUGUAAAAACCAAGAACACAGAUU | 8795 |
| Db | 2391 | GCCGAGCGCATTTGTTTCAATTTCTTGAGTGGGATAGAGCTGAGCAGCCAGCATCGACT | 2450 |
| Qy | 8796 | AGAAAGCAUUUGCGUUCUGAUGAUGAAGCAUUGGGUUUACCCUAGGUUAUCCACGNAU | 8855 |
| Db | 2451 | TGAAGCCATTTGTGCATCTATGATTGAAGCATGGGGTCAACAGGAAATTTATTTGATGAGAT | 2510 |
| Qy | 8856 | UCGAAAUUUUAUGCUUGGGUUCUGGAAACAAAGCACCAUAACAUAUCUCUGCAUCUGAGG | 8915 |
| Db | 2511 | ACGATTTGTTCTACAAATGGGTCAITGAAACAGCACCGTACTCGCAGATCGTATCTGNAGG | 2570 |
| Qy | 8916 | AAAGGCCACCAUA CAUUUCGGAAAACAGCGCUCAAAAGACUUUAACAUCUGGAGAAAGGAAG | 8975 |


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Db 2032 GAATGAAAGAAAG-----AGTCCACGACT 2055
Qy 9282 UAAAUCCGAUUAUCCAAUAAACUCACAAUUGCCAAAGGAAAGGAAUUAUUAUUU 9341
Db 2056 ACAAAAGATAACAAAGAAATGAACCTTCCAAAGTTGGTGGGAAATCATTCTTAGCTT 2115
Qy 9342 GGAGUCCUUUUACAUACACACACAGACUAGGCAUUAUUAUUAUUAUUAUUAUUAU 9401
Db 2116 AGACCATTTGCTCGAGTACAAACCTTAATCAAGTTGATCTGTTTAAACACTCGAGCAACAAA 2175
Qy 9402 UUCACAGUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 9461
Db 2176 AACACAGTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2235
Qy 9462 AAUGGGAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 9521
Db 2236 AATGGGTGTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTGATTG 2295
Qy 9522 CAUUAUUGGCAUUGGUUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 9581
Db 2296 TGTCATATGAGTTTGGGTGATGATGATGATGATGATGATGATGATGATGATGATG 2355
Qy 9582 AAUAGUGGAAAGCAGAAACCCACUUAUUGGCUAGAUUAUUAUUAUUAUUAUUAUUA 9641
Db 2356 AATTGTTGAAATGCAAAACCACTTTAAGACAAATCATGCACATTTCTCAGACGAGC 2415
Qy 9642 UGAAGCAUACAUCAAGAAAGAGAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 9701
Db 2416 AGAAGCATATATTGAATAGAAACTCTGAAAGTCCGTATGATGATGATGATGATGAT 2475
Qy 9702 ACGGAACUCCACCGACAGUAGUUGGCGGAUUAUUAUUAUUAUUAUUAUUAUUAUUA 9761
Db 2476 AAGAAATTTGAGACAGAGGAAATTAGCAGCGTATGCTTTTCACTTTTATGAGGTTA 2535
Qy 9762 AAGGACCGAGCAGCGCGCGGAGCCACUUAUUAUUAUUAUUAUUAUUAUUAUUAU 9821
Db 2536 CAAGACACCTTAATAGGCGAAGAGCAATAGCACAATGAAGCGCGCAGCTCTCGCGG 2595
Qy 9822 UGCGAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 9881
Db 2596 AATTACAGCAGGTTATTGGGCTTGATGATGATGATGATGATGATGATGATGATGAT 2655
Qy 9882 GCGCCACACCGCAGACAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 9923
Db 2656 GAGGCACTGCAAGGACGCGTGAATCAGAAATATGCATATGATGATGATGATGATG 2697

RESULT 14
AA77837
ID AA77837 standard; cdna; 2975 BP.
XX
AC AA77837;
XX
DT 10-AUG-1999 (first entry)
XX
DE WMV2 strain Mar6 3' region cdna.
XX
KW Hammerhead; ribozyme; endoribonuclease activity; catalytic region;
KW potyvirus; replicative strand; viral replication; infection; assembly;
KW cell movement; symptom; resistance; plant; aphid; mite; whitefly;
KW inducible; inhibitor; toxin gene; ss.
XX
OS Watermelon mosaic virus.
XX
PN EF922767-Al.
XX
PD 16-JUN-1999.
XX
PF 03-DEC-1997; 97EP-00402925.
XX
PR 03-DEC-1997; 97EP-00402925.
XX
PA (GENE-) GENE SHEARS PTY LTD.
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Huttner B, Tucker W, Vermeulen A, Ignart F;

WPI; 1999-329398/28.

New ribozyme capable of hybridizing to potyvirus RNA, useful for conferring resistance of plants to potyviral infection.

Example 1; Fig 5A-D; 137pp; English.

This invention describes novel nucleic acid ribozyme molecules with endoribonuclease activity, comprising at least one catalytic region, and at least one hybridizing region which is complementary to at least one target region of the potyvirus genomic (+) and/or replicative (-) strand RNA. The target region does not have a GUC triplet at position 8122-8124 of the PVN strain, or the equivalent triplet of other potyviruses. The ribozyme cleaves potyvirus genomic (+) strand RNA or replicative (-) strand RNA, resulting in reducing viral replication, infection, assembly, cell to cell movement and/or symptoms. The novel ribozyme is useful for providing in vivo resistance to plants against potyviral infection, especially the aphid-, mite- and whitefly transmitted potyviruses, including: Zucchini yellow mosaic virus (ZYMV), Watermelon mosaic virus 2 (WMV2), Tobacco vein mottling virus 2 (TMV2), Tobacco etch virus (TEV), Potato virus Y (PVY), Pepper mottle virus (PePMoV), Soybean mosaic virus (SBMV), Papaya ringspot virus (PRSV), Pea seed-borne mosaic virus (PSBMV), Turnip mosaic virus (TuMV), Johnson grass mosaic virus (JGMV), Plum pox virus (PPV), Maize Dwarf Virus (MDV), Bean common mosaic (BCM), Bean yellow mosaic (BYMV), Carnation vein mottle (CarVMV), Celery mosaic (CeMV), Clover yellow vein (CLYV), Henbane mosaic (HBMV), Lettuce mosaic (LcMV), and Sugarcane mosaic (SCMV) (especially ZYMV and WMV2). An inducible ribozyme gene is useful for inhibiting action of a therapeutic gene if it was necessary, especially useful when using toxin genes, and a synthetic ribozyme could be used to control activity of a therapeutic gene

Sequence 2975 BP; 934 A; 482 C; 721 G; 838 T; 0 U; 0 Other;

Query Match 8.4%; Score 854.8; DB 2; Length 2975;

Best Local Similarity 41.7%; Pred. No. 4.4e-182;

Matches 1144; Conservative 450; Mismatches 1097; Indels 51; Gaps 3;

7182 UAGUUUUUGAACAUCUUGAUUAUAACAACGAGGACAUUGUGGUAUUGCUUUUAGUUA 7241

7 TAGATTCTGGAACATTTGGATACCACTCAAGATGGTTTTTGTGGGCTACCTCTCGTGC 66

7242 UGUCACUGAUGAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 7301

67 TGTCATATGATGATATATTGTTGGTATACATGATTAACATCTAATGATTCAGAGAGAA 126

7302 UUAUUUUCGAAACUUUGACGACGCGUUUGAAGGCGAUUAUUAUUAUUAUUAUUAU 7361

127 TTTCTTTTGTTCATTTTACTGACGGATTGAAACGGAATCTTGAACAATGCTGATAATCT 186

7362 GAAUUGGAGCAGAUUGGACUUAACAACGUUAUUAUUAUUAUUAUUAUUAUUAUUAU 7421

187 GTCGTGGGCAAAACACTGGTTTTTGGGGAACCAAGTAAGATGCGATGGGGCTCTTTGA 246

7422 UCAGGGAUUGUCCCAUGCAAGAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 7481

247 AGTAGAAGAACAGCCCAAGAGAAATTCAGATATCAAACACTCGTGTCTGATCTTTTGG 306

7482 GGAAACCGUGUGCGCUCAGAGUAGCAAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 7541

307 CAACACGGTAGCAGTACAGATAGAA--AAGAGATGGTTTTGGATGCCATGGAAGG 363

7542 AAUUTUGAAGCGGUUGCAACUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 7601

364 GAATTTGATAGCTTGTGTGGCAAGCTGATGCGCAGCTAGTGACAAAGCAGCGTGTAA 423

7602 ACGAUGAUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 7661

424 AAAATGCCCTCATTTTGGCAATATCTTCGTTACATGATGAAGCAAAACAGTCTTTGA 483

Db 2596 AATTACAGCAGGTTATTGGCTTGATGTAATATCTCGACCAATTCCGAAAATACTGA 2655
Qy 9882 GCGCCACACCGCAGACGAUGUUAACCAACACUACUACU 9923
Db 2656 GAGGCACACTGCAAGGCGTGAATCAGATATGCATACTTT 2697

RESULT 15

AAx77839
ID AAX77839 standard; cDNA; 2922 BP.

AC AAX77839;

XX 10-AUG-1999 (first entry)

DT ZYMV strain E15 3' region cDNA.

XX Hammerhead; ribozyme; endoribonuclease activity; catalytic region;
KW potyvirus; replicative strand; viral replication; infection; assembly;
KW cell movement; symptom; resistance; plant; aphid; mite; whitefly;
KW inducible; inhibitor; toxin gene; ss.

XX Zucchini yellow mosaic virus.

XX EP922767-A1.

XX 16-JUN-1999.

XX 03-DEC-1997; 97EP-00402925.

XX 03-DEC-1997; 97EP-00402925.

XX (GENE-) GENE SHEARS PTY LTD.

XX Huttner B, Tucker W, Vermeulen A, Ignart P;

DR WPI; 1999-329398/28.

XX New ribozyme capable of hybridizing to potyvirus RNA, useful for
PT conferring resistance of plants to potyviral infection.

PS Example 1; Fig 6A-D; 137pp; English.

CC This invention describes novel nucleic acid ribozyme molecules with
CC endoribonuclease activity, comprising at least one catalytic region, and
CC at least one hybridizing region which is complementary to at least one
CC target region of the potyvirus genomic (+) and/or replicative (-) strand
CC RNA. The target region does not have a GUC triplet at position 8122-8124
CC of the PVIN strain, or the equivalent triplet of other potyviruses. The
CC ribozyme cleaves potyvirus genomic (+) strand RNA or replicative (-)
CC strand RNA, resulting in reducing viral replication, infection, assembly,
CC cell to cell movement and/or symptoms. The novel ribozyme is useful for
CC providing in vivo resistance to plants against potyviral infection,
CC especially the aphid-, mite- and whitefly transmitted potyviruses,
CC including: Zucchini yellow mosaic virus (ZYMV), Watermelon mosaic virus 2
CC (WMV2), Tobacco vein mottling virus 2 (TMV2), Tobacco etch virus (TEV),
CC Potato virus Y (PVY), Pepper mottle virus (PepMV), Soybean mosaic virus
CC (SBMV), Papaya ringspot virus (PRSV), Pea seed-borne mosaic virus
CC (PSBMV), Turnip mosaic virus (TuMV), Johnson grass mosaic virus (JGMV),
CC Plum pox virus (PPV), Maize Dwarf Virus (MDV), Bean common mosaic (BCMV),
CC Bean yellow mosaic (BYMV), Carnation vein mottle (CarMV), Celery mosaic
CC (CeMV), Clover yellow vein (CLYV), Henbane mosaic (HMV), Lettuce mosaic
CC (LtMV), and Sugarcane mosaic (SCMV) (especially ZYMV and WMV2). An
CC inducible ribozyme gene is useful for inhibiting action of a therapeutic
CC gene if it was necessary, especially useful when using toxin genes, and a
CC synthetic ribozyme could be used to control activity of a therapeutic
CC gene

SQ Sequence 2922 BP; 896 A; 543 C; 708 G; 775 T; 0 U; 0 Other;

Query Match 8.1%;

Best Local Similarity 42.1%; Score 818.2; DB 2; Length 2922;

Matches 1157; Conservative 451; Mismatches 1083; Indels 60; Gaps 8;

Qy 7182 UAGUUUUUGGAAACAUUGGAUUAUAUCAAACGGAAGGACAUUGUGGAUUGCCUUUAGUAG 7241
Db 3 TAGATTCTGGAACAATTGGA-TAACACCAACGAAGGGGATTCGGATTGCCCATGTTTC 61
Qy 7242 UGUCACUGAUGAUUUUUGUAGGAUAUAUAGUUUAUAGUACUAUAGCAUCAUA 7301
Db 62 AACACCGGATGGCAAGATAATTGGAGTTTCATGGTTTGGCTTCCACAGTCTCATCTAAGAA 121
Qy 7302 UUAUUUCUGAACUUUGACGCGUUUGAAGCGGAUUAUUAUAAACAAGUUGAAGGAACU 7361
Db 122 TTATTTTGTCCCATTCCTGATGATTTTATAGCCACGCATTTGAGCACAACCTGATGACCT 181
Qy 7362 GAAUUGGAGCAGAAUUGGACUUAACAAGUUUAUAUUGUUAUGUUGGGCAACAUGAUAU 7421
Db 182 CACATGCACTCAGCATTTGGCTATGGCAACCTAGCAAAATTTGGTGGGAACGCTCAACTT 241
Qy 7422 UCAGGAUUGUGUCUCCCAUGCAAGAAUUAACAACAACAUAAGUUAUAGCGACUUAUGCAC 7481
Db 242 AGTTGATGAACAACACGAGGCCCGCAATTTTCGATTTTCAAAATCTAGTCAAGGATTTATTTCAC 301
Qy 7482 GGAACCCUGUGCGCUCAGAGUAGCAUAUUAAGUUAUUAUUAUUAUUAUUAUUAUUAU 7541
Db 302 TTCTGTGTGTGAACACAG---AGCAAGCGAGAAAGATGGGTCTAGCAAGCTGTGAAG 358
Qy 7542 AAAUUUAAAAGCGGUUCCAAUUAUCCCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 7601
Db 359 GAACCTTCGGGCTGTTGGAACCTGCACATCAGCGTTAGTCACCAACATGTTGTGGAAGG 418
Qy 7602 ACGAUGAAUUUUUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 7661
Db 419 CAAGTGCTCTCTTCGAAAGAATAATTACAAAACACGCAAGAGCGGCGCTATTTCAG 478
Qy 7662 ACCACUGAUGGUUUCUUGGGAAGAGCGUCUCAACAAGGAAGCAUUAUUAAGGACCU 7721
Db 479 ACCCTTAATGGGAGAGTACCGCCGAGCAAGTTGAACAAGAAGAGCTTTAAAGAAGATT 538
Qy 7722 AUUUAUAUAUCACAGAAUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 7781
Db 539 CTTTAAATACAATAAACCCTGCTGTTGTTTAACTGATGATGATGATGATGATGATGATGAT 598
Qy 7782 AGUUGGGCAAGUACUGAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 7841
Db 599 AGTGGATGGGTTATACGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 658
Qy 7842 CGAUUGACCAAGUACUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 7901
Db 659 AGATCCGAGGAGATTACAACTCTTTGAACATGAAGCAGCAATTTGGAGCCCATGATAG 718
Qy 7902 UGUUAGAAAAAGGCGUACUUCGAAAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 7961
Db 719 AGGAAAGAAAGAGTTTTTGGGGGCTAGATGATT-TTGATCGAGAGCGACTTTTATT 777
Qy 7962 GCUUAGUUCUCCGAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 8021
Db 778 CCAAAAGTTGTGAAGAGTTGTTCAATGGCTACAAAGGCTCTGTGGAATGGAATCTTTAAAGC 837
Qy 8022 UGAUUAAGCAAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 8081
Db 838 CGAGCTCAGCGCTTGAGAAAGTCAAGGCTAACAAAACACGAACTTTTACAGCAGCGCC 897
Qy 8082 AAUUGAAACUUUAUUGGCGGAAAGUUUUGCGUGCAUGAUUAUUAUUAUUAUUAUUAUUAUUA 8141
Db 898 AATTGATACATGCTTGGAGCTAAAGTTTGTGTGATGATTTTCAACAATGATGTTCTACAG 957
Qy 8142 UCUUAUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 8201
Db 958 GAAAAACCTCAAGTGTCCATGGACGCTCGCATGCAAAAATTTTATGGTAGTTGGGATAA 1017
Qy 8202 UCUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 8261
Db 1018 ATTGATGAGATCATTTACCTGATGGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1077

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OM nucleic - nucleic search, using sw model

Run on: September 4, 2005, 11:10:24 ; Search time 27840 Seconds
(without alignments)
13884.434 Million cell updates/sec

Title: US-10-076-839A-1

Perfect score: 10155
Sequence: 1 naaaauuaaaacucac.....ucagcuagcaagagggg 10155

Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST.*

1: gb_est1.*
2: gb_est2.*
3: gb_hic.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_gss1.*
9: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|------------|--------------------|
| C 1 | 295.6 | 2.9 | 918 | 7 CV287692 | CV287692 aof01-13m |
| 2 | 289 | 2.8 | 639 | 5 BU760841 | BU760841 sas59d02. |
| 3 | 260.4 | 2.6 | 576 | 2 BF423562 | BF423562 sr37e04.y |
| 4 | 259 | 2.6 | 576 | 5 BQ452872 | BQ452872 ea092e11. |
| 5 | 258 | 2.5 | 579 | 4 BI699497 | BI699497 seg37f04. |
| 6 | 246.8 | 2.4 | 541 | 2 BF423777 | BF423777 sr38h04.y |
| 7 | 246.6 | 2.4 | 475 | 2 BE050823 | BE050823 za69h07.b |
| 8 | 244.8 | 2.4 | 522 | 4 BG882725 | BG882725 sae51g06. |
| 9 | 241.4 | 2.4 | 516 | 4 BG725155 | BG725155 sae33a07. |
| 10 | 239.4 | 2.4 | 569 | 2 BF423490 | BF423490 sr35c03.y |
| 11 | 235 | 2.3 | 510 | 4 BI320765 | BI320765 sae48g02. |
| 12 | 231.6 | 2.3 | 461 | 1 AI372192 | AI372192 au02c06.x |
| 13 | 231.6 | 2.3 | 470 | 2 BE051689 | BE051689 za86h10.g |
| 14 | 230.8 | 2.3 | 521 | 4 BG552477 | BG552477 sad67f10. |
| 15 | 229.4 | 2.3 | 758 | 2 BE820764 | BE820764 GW700012A |
| C 16 | 229 | 2.3 | 677 | 2 BF423735 | BF423735 sr39e05.y |
| 17 | 228.2 | 2.2 | 516 | 2 BE049885 | BE049885 za18f03.f |
| 18 | 226 | 2.2 | 508 | 4 BG651715 | BG651715 sad60a08. |
| 19 | 225 | 2.2 | 516 | 2 BE050782 | BE050782 za69d12.b |
| 20 | 223 | 2.2 | 484 | 4 BG653640 | BG653640 sad76h12. |
| C 21 | 222.8 | 2.2 | 662 | 7 CV045146 | CV045146 EST 6853 |
| 22 | 222.6 | 2.2 | 502 | 4 BG725472 | BG725472 sae37f05. |
| 23 | 222.6 | 2.2 | 518 | 4 BG652025 | BG652025 sad73b07. |
| 24 | 222.4 | 2.2 | 476 | 4 BG653942 | BG653942 sad63c01. |

| | | | | | | |
|----|-------|-----|-----|---|----------|---------------------|
| 25 | 221.8 | 2.2 | 469 | 1 | AI372364 | AI372364 au06b08.x |
| 26 | 221.2 | 2.2 | 485 | 2 | BE051792 | BE051792 za88c02.g |
| 27 | 220.6 | 2.2 | 695 | 6 | CD038767 | CD038767 UTPPI011 |
| 28 | 220.2 | 2.2 | 505 | 4 | BI699184 | BI699184 sag34a02. |
| 29 | 218.6 | 2.2 | 483 | 2 | BE049878 | BE049878 za18d12.r |
| 30 | 218.4 | 2.2 | 477 | 2 | BE051667 | BE051667 za86g10.b |
| 31 | 218.4 | 2.2 | 499 | 4 | BG363345 | BG363345 sac2d0d1. |
| 32 | 218.4 | 2.2 | 565 | 4 | BG359746 | BG359746 sac28b02. |
| 33 | 218.2 | 2.1 | 662 | 2 | BF423648 | BF423648 sr38a08.y |
| 34 | 217.4 | 2.1 | 531 | 4 | BG653691 | BG653691 sad77f05. |
| 35 | 216.8 | 2.1 | 515 | 4 | BI320703 | BI320703 sae47e11. |
| 36 | 213.6 | 2.1 | 469 | 2 | BE058814 | BE058814 sn21c06.y |
| 37 | 212 | 2.1 | 492 | 4 | BG653638 | BG653638 sad76h09. |
| 38 | 211.2 | 2.1 | 432 | 1 | AI372317 | AI372317 au05608.x |
| 39 | 207 | 2.0 | 527 | 4 | BG653970 | BG653970 sad63e10. |
| 40 | 205.2 | 2.0 | 441 | 4 | BG651913 | BG651913 sad62g01. |
| 41 | 204.8 | 2.0 | 461 | 2 | BE051785 | BE051785 za88b05.g |
| 42 | 204 | 2.0 | 509 | 4 | BG653933 | BG653933 sad63b02. |
| 43 | 203.4 | 2.0 | 452 | 2 | BE051668 | BE051668 za86g10.g |
| 44 | 203.2 | 2.0 | 399 | 2 | BE050419 | BE050419 za866d03.b |
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ALIGNMENTS

RESULT 1
CV287692/c
LOCUS CV287692.1 918 bp mRNA linear EST 23-SEP-2004
DEFINITION aof01-13ms4-b08 Aof01 Asparagus officinalis cDNA clone
aof01-13ms4-b08 5', mRNA sequence.
ACCESSION CV287692
VERSION CV287692.1 GI:52570176
KEYWORDS EST.
SOURCE Asparagus officinalis (garden asparagus)
ORGANISM Asparagus officinalis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Asparagales;
Asparagaceae; Asparagus.
REFERENCE 1 (bases 1 to 918)
AUTHORS dePamphilis,C., Carlson,J., Ma,H., Soltis,D., Soltis,P.,
Oppenheimer,D., Frohlich,M., Doyle,J., Tanksley,S., Webb,M.,
Leebens-Mack,J., Landherr,L., Ilut,D. and Wall,K.
TITLE Generation of ESTs from early male inflorescences of Asparagus
officinalis
JOURNAL Unpublished (2004)
COMMENT Contact: Claude dePamphilis or James Leebens-Mack
Penn State University
208 Mueller Laboratory, Department of Biology, ATTN Rm212, Penn
State University, University Park, PA 16802, USA
Tel: 814 863 6413
Fax: 814 865 9131
Email: cwd3@psu.edu or jhl10@psu.edu
The sequence provided is trimmed of vector and low quality regions.
Full sequence and original trace file are available from the Plant
Genome Network website (<http://pgn.cornell.edu>)
Plate: aof01-13ms4 row: b column: 08
Seq primer: M13F.

FEATURES

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/clone="aof01-13ms4-b08"
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/lab_host="SOLR"
/clone_lib="Aof01"
/note="Vector: pBluescript SK (+/-); Site 1: EcoRI;
Site 2: XhoI; This is a directionally cloned,
non-normalized library. This library has been generated by
the Floral Genome Project (FGP). The Floral Genome Project
is funded by NSF's Plant Genome Research Program

Db 361 ATGAGACTGGTGGTGAAGAGAAATCTAGAGAACCTTATGCTGAGATGCTTAC 420
QY 8377 ACCCCCAUUGCAACACUGAUGGAACAGUCGUCAAAAAGUUUCGAGGAAUUAUAGUGGU 8436
Db 421 ACACCAATTTAGCACCTGATGACACAAATTTTAAAGAAGTTTCAGAGGAAACACAGTGG 480
QY 8437 CAACCGUCACAGUCGUAGUAACACAUUGAUGUGUGUUAUUUGUGUGAGUAUUAUUA 8496
Db 481 CAACCAATCTACAGTTGGGCAATACCTTGATGGTAGTCAATCCCATGTAATCTTGT 540
QY 8497 AUUAUGAAUUGUGUAAAGUUUGAAGUACAGAGUAGUCGAGGUAUUUGUUAACGGU 8556
Db 541 TGTAAACAGGTTGGTTCAGAGGAGGACATTCAGAGAAAGATTAGTGGTTTCGCCCATGGC 600
QY 8557 GAUGAUUUUUGUCUUC 8573
Db 601 GATGACATCATCTTGC 617

RESULT 3

BF423562

LOCUS

DEFINITION BF423562 576 bp mRNA linear EST 13-JUL-2004
sr37e04.y1 Gm-c1051 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-c1051-247 5' similar to SW:POLG SBWN P21231 GENOME POLYPROTEIN
[CONTAINS: NUCLEAR INCLUSION PROTEIN B ; mRNA sequence.]

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

BF423562

EST

Glycine max (soybean)

Glycine max

Glycine max

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.

REFERENCE

AUTHORS

1 (bases 1 to 576)
Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Corvelli, V.,
Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.,
Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
McCann, R., Waterston, R. and Wilson, R.
Public Soybean EST Project

TITLE

JOURNAL

COMMENT

Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810

Email: est@watson.wustl.edu

When it has been determined, an EST from the other end of this
clone is listed in the 'Other ESTs on clone' field. This clone is
available through: Biogenetic Services, 801 32nd Ave. Brookings, SD
57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)
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FEATURES

source

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/tissue_type="floral meristematic mRNA"
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/clone_lib="Gm-c1051"
/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:
XhoI; The cDNA library was constructed from floral
meristematic mRNA provided by Dr. Halina Knap of Clemson
University. Complementary DNA was synthesized from mRNA
using a primer consisting of a poly(dT) sequence with a
XhoI restriction site. EcoRI adapters were ligated to the
blunt-ended cDNA fragments followed by XhoI digestion. The

cDNA fragments were directionally cloned into the
EcoRI-XhoI restriction site of the pBluescript vector. The
ligated cDNA fragments were transformed into DH10B host
cells (GibcoBRL). This library was constructed in the
laboratory of Dr. Randy Shoemaker."

ORIGIN

Query Match 2.6%; Score 260.4; DB 2; Length 576;
Best Local Similarity 49.5%; Pred. No. 3.6e-51;
Matches 284; Conservative 94; Mismatches 196; Indels 0; Gaps 0;
QY 9335 UAAUUUGGAGUUCUUUUAACAACACACAGUACAGUAGGACAUUUAUUAUUAUUAUUA 9394
Db 2 TCAGTTTGGACACCTTGGTTGAGTATAAACCTTAATCAGGTGATTATTCATAATCTCGAG 61
QY 9395 CAAAGUAUUUCACAGUUUUAUACAUGGUACAACGUCUGAAGGAAUUAUUAUUAUUAUUA 9454
Db 62 CAAACAAGAACACAAATTCGAAGCGTGGTCAATGCAATGAGTAAAGATGAATATGAGCTTGACG 121
QY 9455 AUGAAGAAUUGGAAUUAUUUAUUGGAUUAUUAUUGUUUGUUUAUUAUUAUUAUUAUUAU 9514
Db 122 ATGAACAGATGGCGGTGTTATCAATGGTTTCATGTTATGTCATCGACAAATGGCACAT 181
QY 9515 CUCCAAACAUAUUAUGGCAUGUUUAUGAUGCAAGGGAAGCAACAUAUUAUUAUUAUUAUUA 9574
Db 182 CTCAGATGCCAATGGCGTGTGGTGATGGATGGAGAAACAGATTGAATATCCGC 241
QY 9575 UUCAACCAUAGUGGAAACCGCAAAACCCACUUUGGUCAGAUUAUUGGUCUACUUUAGCA 9634
Db 242 TGAACCCATTGTCGAGATGCAAAACCACTCTGAGACAAATATGACCACCTTCTCAG 301
QY 9635 AUGUUGCAAGCAUACUACGAAAAAGAGAAUUAUUGAAGCAUUAUUGCCGAGUACG 9694
Db 302 ATGCAGCAGAGCTTACATTGAGATGAGAAATTCGAAAGTCGTTATATATGCTAGATATG 361
QY 9695 GUUAUCAAGCAACCUACCGCAGUAGUUUGCGCAUUGUUUGAUUUUAUUAUUAUUAUUA 9754
Db 362 GACTACTGAGGAATTTGAGAGATAGAGACTAGCCGCTATGCTTTGATTCTTATGAGG 421
QY 9755 UGACAUCAAGGACGCGCAGCUGCGGCGCGGAGCCCAUUAUUAUUAUUAUUAUUAUUAU 9814
Db 422 TTACTTCCAAACACCAACACGCGCAAGGAGCAATAGCCGAGATGAAGGCTGCAGCTC 481
QY 9815 UCGGAGUUCGAAUUAUUAAGAUUUUGGACUGGAGGAAUUAUUGGAGGAAUUAUUGGAG 9874
Db 482 TTTCCGGAGTTAAACAAGTTGTTGGACTTGTGAGGAAACATCTCAACTAATCCGATG 541
QY 9875 ACACGAGCGCCACACCGCGCAGCAUGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 9908
Db 542 ATACTGAAAGGCACACTGCATGGGATGTGAATCA 575

RESULT 4

BQ452872

LOCUS

DEFINITION

BQ452872

576 bp mRNA linear

EST

Glycine max cDNA clone

SOYBEAN CLONE ID:

Gm-c1081-3286 5' similar to SW:POLG SBWN P21231 GENOME POLYPROTEIN

[CONTAINS: NUCLEAR INCLUSION PROTEIN B ; mRNA sequence.]

BQ452872

GI:21255984

Glycine max (soybean)

Glycine max

Glycine max

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;

Glycine.

1 (bases 1 to 576)

Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Corvelli, V.,

Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,

Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.,

Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,

Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,

| | | | |
|----------|------|---|------|
| TITLE | | McCann,R., Waterston,R. and Wilson,R. | |
| JOURNAL | | Public Soybean EST Project | |
| COMMENT | | Unpublished (1999) Contact: Shoemaker R/Public Soybean EST Project Public Soybean EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu When it has been determined, an EST from the other end of this clone is listed in the 'Other ESTs on clone' field. This clone is available through: Biogenetic Services, 801 32nd Ave. Brookings, SD 57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com) Seq primer: -40RP from Gibco High quality sequence stop: 426. Location/Qualifiers | |
| FEATURES | | 1..576 /organism="Glycine max" /mol_type="mRNA" /cultivar="Bragg" /db_xref="taxon:3847" /clone="SOYBEAN CLONE ID: Gm-cl081-3286" /tissue_type="Roots of 7 day old 'Bragg' seedlings" /dev_stages="7 days old" /lab_host="DH10B" /clone_lib="Gm-cl081" /note="Vector: pBluescript II SK+; Site: 1: EcoRI; Site: 2: XhoI; The mRNA was isolated from roots of 7 day old 'Bragg' seedlings that were mock-infected 48 hours prior to harvest. Dr. Gary Stacey generously donated the tissue. The roots were flash-frozen in liquid nitrogen. Stratagene's cDNA Synthesis Kit (catalog number 200401) was used to synthesize the cDNA. First-strand synthesis was performed with 5-methyl dCTP, hence the ligated cDNA was hememethylated. A modification of Stratagene's first-strand synthesis primer was used. An 'anchor' nucleotide (V=A, C, or G) was added to the 3' end of the primer (GAGAGAGAGAGAGAGAGAACTAGTCTCGAG(T)18V) to anchor the primer at the 5' end of the poly(A) tract. After second-strand synthesis, the cDNA ends were filled in with cloned Pfu DNA, ligated to EcoRI adapters and subsequently phosphorylated. The cDNA was then precipitated and redissolved in sterile, RNase-, DNase-free water. The XhoI site within the first- strand synthesis primer was then restricted by digestion with XhoI from Promega (40U/ul); all XhoI sites in the cDNA would be protected by their hememethylated status. The cDNA constructs were size-fractionated with a 500bp cutoff, using Sephacryl S-500 High Resolution (Pharmacia Biotech) in a 2-mm diameter column and a bed volume of approximately 1ml. The column eluent was precipitated, redissolved, and ligated into Stratagene's pBluescript II XR Predigested vector (pBluescript II SK(+)) vector that has been digested with EcoRI and XhoI, and phosphorylated by Stratagene). This library was constructed in the laboratory of Dr. Paul Keim and Dr. Virginia H. Coryell at Northern Arizona University." | |
| ORIGIN | | Query Match 2.6%; Score 259; DB 5; Length 576; Best Local Similarity 48.9%; Pred. NO. 7.8e-51; Matches 279; Conservative 97; Mismatches 195; Indels 0; Gaps 0; | |
| QY | 9288 | GAUAUCCAAUAACUACAUAUGCCAAAGGAAAGGAAAGAAUUAUUUAUUUGAGUU | 9347 |
| Db | 3 | GATTACAAGGAGATGAATCTTCCAATGGTTGAAGGGAAGATCATCTCGATTGGACCA | 62 |
| QY | 9348 | CCUUUUAUAUAACACCAACGAGUAGGCAUUAUCAAUAACACGAGCGCAAGUAUUCAC | 9407 |
| Db | 63 | CTTGTCTTGGTATCAAAACCTTAATCAGGTGATTTTATTCAACATCTGAGCAACAAGACA | 122 |
| QY | 9408 | GUUUAUAUACAUAGGUACAACCGUGUAGGAUAUCCUUAUGGUGUGUCUGAUGAAGAAUGGG | 9467 |

| | | |
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| QY | 9709 | CUCACCCGACAGUAGUUUGCGCGCAUGAUUGCUUUUUAUU |
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Db 481 AATACTGAAAGGCACACTCGAAGGATGTGAATCAAAACA 520

RESULT 9
 BG725155
 LOCUS
 DEFINITION
 ID: Gm-cl051 Glycine max cDNA clone GENOME SYSTEMS CLONE
 ID: Gm-cl051-6925 5' similar to SW:POLG SBMVN P21231 GENOME
 POLYPROTEIN [CONTAINS: NUCLEAR INCLUSION PROTEIN B ;, mRNA
 sequence.
 BG725155
 BG725155.1 GI:14008551
 EST.
 SOURCE
 Glycine max (soybean)
 ORGANISM
 Glycine max
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; lea-
 rosids; eurosids 1; Fabales; Fabaceae; Papilionoideae; Phaseoleae
 Glycine.
 1 (bases 1 to 516)
 Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Corvelli,V.,
 Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J.,
 Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M.,
 Bowers,X., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N.,
 Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
 McCann,R., Waterston,R. and Wilson,R.
 Public Soybean EST Project
 Unpublished (1999)
 TITLE
 JOURNAL
 COMMENT
 Contact: Shoemaker R/Public Soybean EST Project
 Public Soybean EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.wustl.edu
 When it has been determined, an EST from the other end of this
 clone is listed in the 'Other ESTs on clone' field. This clone is
 available through: Biogenetic Services, 801 32nd Ave. Brookings, SD
 57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)
 High quality sequence stop: 414.
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 XhoI; The cDNA library was constructed from floral
 meristematic mRNA provided by Dr. Halina Knap of Clemson
 University. Complementary DNA was synthesized from mRNA
 using a primer consisting of a poly(dT) sequence with a
 XhoI restriction site. EcoRI adapters were ligated to the
 blunt-ended cDNA fragments followed by XhoI digestion. The
 cDNA fragments were directionally cloned into the
 EcoRI-XhoI restriction site of the pBluescript vector. The
 ligated cDNA fragments were transformed into DH10B host
 cells (GibcoBRL). This library was constructed in the
 laboratory of Dr. Randy Shoemaker."

ORIGIN

Query Match 2.4%; Score 241.4; DB 4; Length 516;
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QY 9367 GAUCAAGUGCAUUCAAUACACGAGCAAGUUUUCACAGUUUAUACAGUGCAAC 9426

Db 1 GATCAGGTGTATTATTCACACTCGAGCAACAGAACACAGTTCGAGCGTGGTACAT 60


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RESULT 10

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BF423490
LOCUS
DEFINITION
sr35c03.y1 Gm-cl051 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-cl051-29 5', similar to SW:POLG.SBMVN P21231 GENOME POLYPROTEIN
[CONTAINS: NUCLEAR INCLUSION PROTEIN B i, mRNA sequence.

ACCESSION
BF423490
VERSION
BF423490.1 GI:11411479
KEYWORDS
EST.
SOURCE
Glycine max (soybean)
ORGANISM
Glycine max
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 569)
REFERENCE
Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Corvett,V.,
Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J.,
Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M.,
Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N.,
Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
McCann,R., Waterston,R. and Wilson,R.
Public Soybean EST Project
Unpublished (1999)
CONTACT: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
When it has been determined, an EST from the other end of this
clone is listed in the 'Other ESTs on clone' field. This clone is
available through: Biogenetic Services, 801 32nd Ave. Brookings, SD
57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)
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High quality sequence stop: 359.
Location/Qualifiers
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/organism="Glycine max"
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FEATURES

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/db_xref="taxon:3847"
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/tissue_type="floral meristematic mRNA"
/lab_host="DH10B"
/clone_lib="Gm-cl051"
/notes="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:
XhoI; The cDNA library was constructed from floral
meristematic mRNA provided by Dr. Halina Knap of Clemson
University. Complementary DNA was synthesized from mRNA
using a primer consisting of a poly(dT) sequence with a
XhoI restriction site. EcoRI adapters were ligated to the
blunt-ended cDNA fragments followed by XhoI digestion. The
cDNA fragments were directionally cloned into the
EcoRI-XhoI restriction site of the pBluescript vector. The
ligated cDNA fragments were transformed into DH10B host
cells (GibcoBRL). This library was constructed in the
laboratory of Dr. Randy Shoemaker."
```

ORIGIN

```
Query Match 2.4%; Score 239.4; DB 2; Length 569;
Best Local Similarity 48.3%; Pred. No. 4.le-46;
Matches 267; Conservative 90; Mismatches 196; Indels 0; Gaps 0;

QY 9380 UUCAAAUACCAAGGCGCAAGUAUUUCACAGUUUAUACAUGGUACAAACGUCUGAAGGAU 9439
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 4 TATTCAATACTCGAGCAACAAGACACAGATTTTGAGGCTGTGTACATGTCAGTTAAAGATG 63

QY 9440 CCUAGUGUGUGUCUGAUGAAGAAUUAUUUGAAUGGAUUAUUGGUUGUGUGUA 9499
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 64 AATATGAATTTGATGATGAGCAGATGGTGTGTCATGAATGTTTCATGTTATGTTGCA 123

QY 9500 UGAAAAUGGAACAUCUCCAAACAUAUUAUGGCAUGUUGUUUAUGCAAGCGGGAAGAAC 9559
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 124 TTGATAATGGCAGCTCTCCAGATGCCAATGGTGTGTGGGTAAATGATGATGGAGGGAAC 183

QY 9560 AAUUGGAAUACCCCUCAACCAUAGUGGAAACCGCAAAACCCACUUGGUCAGAUUA 9619
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 184 AGATTGAATATCCACTGAAGCCCATCGTTGAATAATGCAAAACCAACTTTGAGGCAATCA 243

QY 9620 UGGCUCACUUUAGCAUUGUGAAGCAUACAUCGAAAGAGAAUUAUUGAAGAGCAU 9679
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 244 TGCACCAATTTTCAGATGCAGCAGAGCTTACATTGAGATGAGAAATCTGAAAGTCGT 303

QY 9680 AUUUGCCGAGUACGUAUUAUACAAGAACCUACCGACCAUGAGUUUGCGGCAUUGCU 9739
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 304 ATATGCTTAGATATGGACTACTGAGGAATTTGAGAGATAGAGATTAGCCGTTATGCT 363

QY 9740 UUGAUUUAUUGAAUAGCAUACAAGGACCGCAGCUGCGGCCCGGGAAGCCCAUCCAGA 9799
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 364 TTGATTTCTATGAGTCACTCCAAACACCGAACAGGCGCAAGGAGCAATAGCACAA 423

QY 9800 UGAAAGCUGCAGCAUUGCGAGAUUGGAAUUAUUAUUGAUGUUGGACUGGAAGAAUGCG 9859
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 424 TGAAGGCTGCAGCTCTCTCGGAGTTAAACAACAGCTGTTTGGGCTTGATGAAACATCT 483

QY 9860 GAAUGCGACUGAGAACACGAGCGCCACACCGCAGCAUGUUAUACCAUACACUCUAUG 9919
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 484 CGACCAACTCCGAAATAATCTTGAAGGCCACACTGCAAGAGATGTGAAATCATACATGCATA 543

QY 9920 CAUUCACCGCGGU 9932
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 544 CTCCTCTGGGCAT 556
```

RESULT 11

```
BI320765
LOCUS
DEFINITION
sae48g02.y3 Gm-cl051 Glycine max cDNA clone GENOME SYSTEMS CLONE
ID: Gm-cl051-8380 5', similar to SW:POLG.SBMVN P21231 GENOME
POLYPROTEIN [CONTAINS: NUCLEAR INCLUSION PROTEIN B i, mRNA
sequence.

BI320765 510 bp mRNA linear EST 21-JUL-2004
```

[illegible]

Tel: 314 286 1800
Fax: 314 286 1810
Email: estewartson.wustl.edu
When it has been determined, an EST from the other end of this clone is listed in the 'Other ESTs on clone' field. This clone is available through: Biogenetic Services, 801 32nd Ave. Brookings, SD 57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)
High quality sequence stop: 394.

FEATURES
source

```

1. 521
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Corolla"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-C1051-5276"
/tissue_type="floral meristematic mRNA"
/lab_host="DH10B"
/clone_lib="Gm-C1051"
/note="Vector: pBluescript II SK+; Site1: EcoRI; Site_2:
XhoI; The cDNA library was constructed from floral
meristematic mRNA provided by Dr. Halina Knap of Clemson
University. Complementary DNA was synthesized from mRNA
using a primer consisting of a poly(dT) sequence with a
XhoI restriction site. EcoRI adapters were ligated to the
blunt-ended cDNA fragments followed by XhoI digestion. The
cDNA fragments were directionally cloned into the
EcoRI-XhoI restriction site of the pBluescript Vector. The
ligated cDNA fragments were transformed into DH10B host
cells (GibcoBRL). This library was constructed in the
laboratory of Dr. Randy Shoemaker."

```

ORIGIN

Query Match 2.3%; Score 230.8; DB 4; Length 521;
Best Local Similarity 48.2%; Pred. No. 4.8e-44;
Matches 248; Conservative 89; Mismatches 177; Indels 0; Gaps 0;

| | | |
|------|---|------|
| 9288 | GAUUAUCAAUAAACUCACAUAUGCCAAAAGUGAAAGGGAAGAAUUUUAAUUUGAGUUU | 9347 |
| Qy | | |
| 8 | GATTACAAGGAAGATGAATCTTCCAATGGTTGAAGGGAAGATCATCTCAGTTTGGACCA | 67 |
| Db | | |
| 9348 | CCUUUUAUAUAUACACACACAGAACUGGACAUUUCAAUAAACAGGCGCAAGUAUUUCACA | 9407 |
| Qy | | |
| 68 | CTTGCTTGAGTACAAACCTTAATCAGGTGTGAATTATTCAACACCTCGAGCAACAAGAACACA | 127 |
| Db | | |
| 9408 | GUUUAUAUAUAUGGUACAAACGUCUGUAAGGAUUCUUAUGGUGUCUGUAUGCAAGAAUUGG | 9467 |
| Qy | | |
| 128 | GTTTCGAAGCGTGGTGCACATGCAGCTTAAGATGAATATGACCTTGACGATGACGATGGG | 187 |
| Db | | |
| 9468 | AAUAAUUUUAAUUGGAUUAAUUGGUUUUGUGUAUUGAAAUUGGAACAUUCUCAAACAUA | 9527 |
| Qy | | |
| 188 | TGTGGTTATGAATGGTTTCATGTGTATGGTGCATTGACAATGGGCACATCTCCAGATGCTAA | 247 |
| Db | | |
| 9528 | UGGCAUGUGUUUAUAUGCAAGGCGGAGAGAAACAAUUGCGAAUACCCCUUCAAACCAUAGU | 9587 |
| Qy | | |
| 248 | TGC CGTGTGCGGTGATGATGGAATGGATGGAGGAGCAACAGATTGAATATCCGCTGAACCCCATTTGT | 307 |
| Db | | |
| 9588 | GGAAACGCAAAACCCACUUTUGCGUCAGAUUAUGGCUCUACUUAGCAUAUGUUCUGCAAGC | 9647 |
| Qy | | |
| 308 | CGAAATATGCAAAACCAACTTTTGAGACAAATATGCAACCATTTCTCAGATGCAGCAGAAGC | 367 |
| Db | | |
| 9648 | AUACAUCGAAAAGAGAAAUUAUCAGAAAGCCAAUAUUGCCGAGGUACGGUAUUAACACGGAA | 9707 |
| Qy | | |
| 368 | TTACATTGAGATGAGAAATTCGAAAGTCGGTATATGCCTAGATATGGACTACTTGAGGAA | 427 |
| Db | | |
| 9708 | CCUACCCGACAUGAGUUUGGCGCGCAUAUGCUUUUGUAUUUCUAUUGAAAUUGCAUCAAGGAC | 9767 |
| Qy | | |
| 428 | TTTGTGAGATAGAGAGCTAGCTCGCTATGCTTTTGATTTCTATGAGGTTACTTCTTAAAC | 487 |
| Db | | |
| 9768 | GCGAGCUCGCGGCCGGAGGCCCAUCCAGAU | 9801 |
| Qy | | |
| 488 | ACCAAAACAGGCAAGGGAAGCAATAGCGCAGATG | 521 |
| Db | | |

488 ACCAAAACAGGCAAGGAAGCAATAGCGCAGATG 521

[illegible]

ORIGIN

Query Match 2.3%; Score 229.4; DB 2; Length 758;
Best Local Similarity 49.5%; Pred. No. 1.2e-43;
Matches 252; Conservative 80; Mismatches 177; Indels 0; Gaps 0;

| | |
|------------|--|
| RESULT 15 | |
| BE820764/c | |
| LOCUS | |
| DEFINITION | |

| | |
|------------|-----------------------|
| DEFINITION | mRNA sequence. |
| ACCESSION | BE820764 |
| VERSION | BE820764.1 |
| KEYWORDS | EST. |
| SOURCE | Glycine max (soybean) |
| ORGANISM | Glycine max |

REFERENCE AUTHORS

| TITLE | JOURNAL | COMMENT |
|---|---------------------------------|-----------------------------------|
| 1. The Role of the Teacher in the Classroom | Journal of Educational Research | 1980, Vol. 83, No. 1, pp. 1-10 |
| 2. The Impact of Technology on Education | Journal of Educational Research | 1980, Vol. 83, No. 2, pp. 11-20 |
| 3. The Importance of Parental Involvement | Journal of Educational Research | 1980, Vol. 83, No. 3, pp. 21-30 |
| 4. The Effect of Teacher Expectations on Student Achievement | Journal of Educational Research | 1980, Vol. 83, No. 4, pp. 31-40 |
| 5. The Role of the School in the Community | Journal of Educational Research | 1980, Vol. 83, No. 5, pp. 41-50 |
| 6. The Impact of Socioeconomic Status on Student Achievement | Journal of Educational Research | 1980, Vol. 83, No. 6, pp. 51-60 |
| 7. The Importance of Teacher Education | Journal of Educational Research | 1980, Vol. 83, No. 7, pp. 61-70 |
| 8. The Effect of Teacher Attitudes on Student Achievement | Journal of Educational Research | 1980, Vol. 83, No. 8, pp. 71-80 |
| 9. The Role of the School in the Community | Journal of Educational Research | 1980, Vol. 83, No. 9, pp. 81-90 |
| 10. The Impact of Socioeconomic Status on Student Achievement | Journal of Educational Research | 1980, Vol. 83, No. 10, pp. 91-100 |

Other ESTs: AW453391 corresponding to Gm-c1016-5630 (5')
Contact: Vodkin, L.O., PI, A Functional Genomics Program for
Soybean (NSF 9872565)
Lewin, H. A., Director, Keck Center for Comparative and Functional
Genomics
University of Illinois
Edwin R. Madigan Building, 1201 W. Gregory, Urbana, IL 61801, USA
Tel: (217) 248-6147
Fax: (217) 333-4582
Email: l-vodkin@uiuc.edu
This clone is available through: Genome Systems, Inc. 4633 World
Parkway Circle St. Louis, Missouri 63134. For further information
call: (800) 430-0030 or (314) 427-3222 FAX: (888) 919-3324 or (314)
427-3324 or contact: clones@genomesystems.com or info@genome
systems.com web site: www.genomesystems.com
Seq primer: 5'-TTTTTTTTTTTTTTTTT(A/C/G)-3'.

FEATURES

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/organism="Glycine max"
/mol_type="mRNA"
/db_xref="taxon:3847"
/clones="Gm-r1070-4946"
/clone_lib="Gm-r1070"
/note="The library Gm-r1070 is a sequence-driven, reracked set of 9,216 clones selected from cDNA libraries from various tissues and stages of development of soybean that represent 2,639 sequences from immature cotyledons, 1,770 from immature seed coats, 3,938 from flowers, and 869 from young pods. The 5' ESTs of the source clones from the different libraries was used to select singletons, or a representative of each contig, which were reracked to form library Gm-r1070. The cDNA clones of the reracked Gm-r1070 library were then sequenced at the 3' end. The contig analysis to select unique genes was performed by the laboratory of Ernest Retzel, Center for Computational Genomics and Bioinformatics, University of Minnesota, http://www.cbc.umn.edu/ResearchProjects/Soybean/Index.html. Reracking was performed by Genome Systems, St. Louis, http://www.genomesystems.com, and 3' sequencing by the Keck Center for Comparative and Functional Genomics, University of Illinois, http://www.life.uiuc.edu/biotech/keck.html. Note: The corresponding 5' EST from each clone in the Gm-r1070 library is listed in the 'OTHER EST' field. The detailed information on the source library for each clone can also be obtained by referring to the Genome Systems clone ID of the original cDNA library that is also listed under 'OTHER EST'."

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2.38; Score 229.4; DB 2; Length 758;

2.5%; SCORE 225.4; DB 2; length 138;
 identity 49.5%; Pred. No. 1.2e-43;
 conservative 80; Mismatches 177; Indels 0; Gaps 0;

